

Mon Jun 2 08:44:23 2003

us-10-005-469-4.rge

Page 1

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2003, 20:03:04 ; Search time 13027 Seconds

(without alignments)
17854.427 Million cell updates/sec

Title: US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagcccccagatgggggc.....ctctctgcagatcaagtact (7992)

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :
1: gb_ba :
2: gb_htg :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pat :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sts :
12: gb_sy :
13: gb_un :
14: gb_vi :
15: em_ba :
16: em_fun :
17: em_hum :
18: em_in :
19: em_mu :
20: em_om :
21: em_or :
22: em_ov :
23: em_pat :
24: em_ph :
25: em_pl :
26: em_ro :
27: em_sts :
28: em_un :
29: em_vi :
30: em_htg_hum :
31: em_htg_inv :
32: em_htg_other :
33: em_htg_mus :
34: em_htg_pln :
35: em_htg_rtd :
36: em_htg_mam :
37: em_htg_vrt :
38: em_sy :
39: em_htgo_hum :
40: em_htgo_mus :
41: em_htgo_other :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	7982.6	99.9	7989 6 AX036255	AX036255 Sequence
2	7982.6	99.9	7989 12 SSR242652	AJ242652 Hepatitis
3	7960.6	99.6	8001 6 AX036254	AX036254 Sequence
4	7960.6	99.6	8001 12 SSR242654	AJ242654 Hepatitis
5	7943	99.4	8001 6 AX036257	AX036257 Sequence
6	7941.4	99.4	8001 6 AX036257	AX036257 Sequence
7	7935	99.3	8001 6 AX036261	AX036261 Sequence
8	7324.6	91.6	8637 6 AX036253	AX036253 Sequence
9	7324.6	91.6	8637 12 SSR242651	AJ242651 Hepatitis
10	7302.6	91.4	8649 6 AX036256	AX036256 Sequence
11	7302.6	91.4	8649 12 SSR242653	AJ242653 Hepatitis
12	7267.4	90.9	8639 6 AX472291	AX472291 Sequence
13	7266.4	90.9	8638 6 AX472314	AX472314 Sequence
14	7246.6	90.7	8638 6 AX472297	AX472297 Sequence
15	7245.6	90.7	8638 6 AX472315	AX472315 Sequence
16	7242	90.6	8642 6 AX472292	AX472292 Sequence
17	7239.2	90.6	8638 6 AX472296	AX472296 Sequence
18	7223.4	90.4	8648 6 AX472295	AX472295 Sequence
19	7219.4	90.3	8643 6 AX472294	AX472294 Sequence
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23	6161.2	77.1	11076 6 AX036258	AX036258 Sequence
24	6154.8	77.0	11076 6 AX036262	AX036262 Sequence
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39	5315.2	66.5	9595 14 AF054248	AF054248 Hepatitis
40	5312	66.5	9595 6 AR119832	AR119832 Sequence
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44	5304.8	66.4	9580 14 AF054250	AF054250 Hepatitis
45	5304	66.4	9373 14 AF208024	AF208024 Hepatitis

ALIGNMENTS

RESULT 1	AX036255	7989 bp	DNA	linear	PAT 16-NOV-2000
LOCUS	AX036255				
DEFINITION	Sequence 4 from Patent EP1043399				
ACCESSION	AX036255				
VERSION	AX036255.1	GI:11225871			
KEYWORDS					
SOURCE	Hepatitis C virus.				
ORGANISM	Hepatitis C virus.				
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;					
Hepatitis C virus.					
REFERENCE	1 (bases 1 to 7989)				
AUTHORS	Bartenschlager, R.D.				
TITLE	Hepatitis C virus cell culture system				
JOURNAL	Patent: EP 1043399-A 4 11-OCT-2000;				

FEATURES BARTENSCHLAGER RALF DR (DE)
Location/Qualifiers
Source 1. 7989
/organism="Hepatitis C virus"
/db_xref="taxon:11103"
BASE COUNT 1647 a 2368 c 2243 g 1731 t
ORIGIN

Query Match 99.98; Score 7982.6; DB 6; Length 7989;
Best Local Similarity 99.98; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 3 GCCAGCCCCCATTTGGGGGGGACACCTCCACATAGATCACTCCCTGTGGAAGTACTG 60
QY 61 TCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTGTCAGCTCCAGAGAC 120
DB 61 TCTTCACGCAAAAGCGTCTAGCCATGGCGTTAGTATGATGTGTCAGCTCCAGAGAC 120
QY 121 CCCCCCTCCGGGAGAGCATAGTGTGCGGAACCGGTGAGACACCGGAATTGCGAG 180
DB 121 CCCCCCTCCGGGAGAGCATAGTGTGCGGAACCGGTGAGACACCGGAATTGCGAG 180
QY 181 GACGACCGGGTCCTTTCTTGATCAACCCCGTCATGCTGAGAGATTTGGGCGCTGCC 240
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DB 241 GCGAAGCTAGCGAGATAGTGTGGTGGCGAAAGCGCTGTGACTGCTGATAGG 300
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QY 661 TCGTATTTGGGCGAAGTGGCGGGGCGAGATCTCTGTATCTACCTTGTCTGCGGAGA 720
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DB 1081 TTGGGCGGGAATGGGCTGACCGCTTCTGCTGTTACGATATGCGCGCTCCGATTTGCG 1140
QY 1141 AGCGATGCGCTTCTATCGCTTCTTGACAGTTCCTTGAAGTTAAGACACACAG 1200
DB 1141 AGCGATGCGCTTCTATCGCTTCTTGACAGTTCCTTGAAGTTAAGACACACAG 1200
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DB 1201 GTTCCCTCTAGCGGATCAATTCCGCCCTCCCTCCCGCCCGCCCTTAAGTTACTGCG 1260
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DB 1261 CGAAGCGCTTGAATAGAGCGGCTGTGCTGTCTATATGTTATTTTCACCATATTG 1320
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DB 1321 CCGTCTTTTGGCAATGTGAGGGCGGGAACCTGACCTCTCTTGTGACGACATTCCT 1380
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DB 1381 AGGGTCTTTCCTCTGCGCAAGAGATGCAAGTCTGTGATGTCGGAAGAGAGA 1440
QY 1441 GTTCTCTGSAAGCTTCTGTAAGACAAACAGCTGTAGCGACCTTTCAGAGCGAGG 1500
DB 1441 GTTCTCTGSAAGCTTCTGTAAGACAAACAGCTGTAGCGACCTTTCAGAGCGAGG 1500
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DB 1501 AACCCCGACCTGGCGACAGGTGCTCTCGGGCCAAAGCCAGCTGATATGATACCT 1560
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DB 1561 GCAAGGGCGGACAAACCCAGTGGCAGCTGTGATGATGATGTTGGAAGATCAAA 1620
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QY 2101 GCGAGCTCGGACCTTACTTGTGTACAGAGGATGCGGATGTGATTCGCGTGC 2160
Db GCGAGCTCGGACCTTACTTGTGTACAGAGGATGCGGATGTGATTCGCGTGC 2160
QY 2161 GCGAGCAGAGGGGGAGGCTTACTTCCCGCAGAGCGCGTCTCTACTTGAAGAGCTTTCG 2220
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QY 2221 GCGAGCTCAGTCTGTGCCCTCGGGGACAGCTGTGGGATCTTTCGCGCTGC 2280
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QY	4621	GAGGACTGCTCACGCGCATGCTCCGGCTGTGAGCTTAAGAGATGTTTGGGATTTGATATGC	4680
Db	4621	GAGGACTGCTCACGCGCATGCTCCGGCTGTGAGCTTAAGAGATGTTTGGGATTTGATATGC	4680
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QY	5041	ACCACTGCAACGTTAAGTCCCGGTGTCAAGGTTCCGGCCCCCGAATTTCTTACAGAAAGTG	5100
Db	5041	ACCACTGCAACGTTAAGTCCCGGTGTCAAGGTTCCGGCCCCCGAATTTCTTACAGAAAGTG	5100
QY	5101	GATGGGGTGGGTGTGACAGGTTACGTCGCAAGCGTGTCAAAAGCCCTCTTACGGGAGAGGTC	5160
Db	5101	GATGGGGTGGCGGTGTGACAGGTTACGTCGCAAGCGTGTCAAAAGCCCTCTTACGGGAGAGGTC	5160
QY	5161	ACATTCCGTGTGGGCTCAATCAATACCTGTGGGTCAAGCTCCCATGCGAGGCCGAA	5220
Db	5161	ACATTCCGTGTGGGCTCAATCAATACCTGTGGGTCAAGCTCCCATGCGAGGCCGAA	5220
QY	5221	CGGAGCGTAGAGAGTGTCACTTCCATGCTCAACGACCCCTCCCATTAACGGCGAGAGCG	5280
Db	5221	CGGAGCGTAGAGAGTGTCACTTCCATGCTCAACGACCCCTCCCATTAACGGCGAGAGCG	5280
QY	5281	GCTAAGCGCTAGGCTTGGCCAGGGGATCTCCCTCTTGGCCAGCATCACTATAGCCAG	5340

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Bartenschlager, R., Korner, F., Koch, J., Herian, U., Theilmann, L. and Bartenschlager, R.
TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
JOURNAL Science 285 (5424), 110-113 (1999)
MEDLINE 99322193
PUBMED 10390360
REFERENCE 2 (bases 1 to 7989)
Bartenschlager, R.
AUTHORS Direct Submission
JOURNAL Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY
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Db	1861	AGCCTCACAGCCGGGACAGAACACAGATCGAAGGGGAGTCCAGTGTCTCCACCGCA	1920
Qy	1921	ACACATCTTTCCTGGCGACTGCTGCAATGGCGTGTGTGGACTGTCTATCATGTGTC	1980
Db	1921	ACACATCTTTCCTGGCGACTGCTGCAATGGCGTGTGTGGACTGTCTATCATGTGTC	1980
Qy	1981	GGCTCAAGAGCCCTTGGCGGCCCAAGAGGCCAATCACCAATGTACACCAATGTGAC	2040
Db	1981	GGCTCAAGAGCCCTTGGCGGCCCAAGAGGCCAATCACCAATGTACACCAATGTGAC	2040
Qy	2041	CAGGACCTCGTCGGCTGGCAAGGCCGCCCGGGGGCGCGTTCCCTGACACCATGACCTGC	2100
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Db	2101	GGCAGCTCGGACCTTACTTGTGCACAGAGCAATGCCGATGTCATCCGCTGCGCGGGG	2160
Qy	2161	GGCACAAGAGGGGAGGACCTACTCTGCCAGGCCCGTTCCTACTTAAGGGCTCTTCG	2220
Db	2161	GGCACAAGAGGGGAGGACCTACTCTGCCAGGCCCGTTCCTACTTAAGGGCTCTTCG	2220
Qy	2221	GGCGGTCCACTGCTCTCCCTCGGGGACACGCTGTGGCATCTTTCGGGCTGCCGTGTGC	2280
Db	2221	GGCGGTCCACTGCTCTCCCTCGGGGACACGCTGTGGCATCTTTCGGGCTGCCGTGTGC	2280
Qy	2281	ACCAGAGGGTGTGGAAGGCGGTGACTTTGTACCCGCTGACTCATATGAAACCACTATG	2340
Db	2281	ACCAGAGGGTGTGGAAGGCGGTGACTTTGTACCCGCTGACTCATATGAAACCACTATG	2340
Qy	2341	CGGTCCCCGCTTTCACGGACAACCTGTCCTCCGCGCGGTACCCGAGACATTTCCAGGTG	2400
Db	2341	CGGTCCCCGCTTTCACGGACAACCTGTCCTCCGCGCGGTACCCGAGACATTTCCAGGTG	2400
Qy	2401	GCCCATCTACAGCCCTACTGCTAGCGGAAGGGAAGACATTAAGTGCCTGGCTCCGTATCA	2460
Db	2401	GCCCATCTACAGCCCTACTGCTAGCGGAAGGGAAGACATTAAGTGCCTGGCTCCGTATCA	2460
Qy	2461	GCCCAAGGTTAAGTGTCTGTCTGAACCCGCTCCGTCGCCGCAACCTAGTTCGGG	2520
Db	2461	GCCCAAGGTTAAGTGTCTGTCTGTGAACCCGCTCCGTCGCCGCAACCTAGTTCGGG	2520
Qy	2521	GGCTATATGTATAGGACATGTGTATGCAACCTAATAGAAACCGGGTAAAGACATC	2580
Db	2521	GGCTATATGTATAGGACATGTGTATGCAACCTAATAGAAACCGGGTAAAGACATC	2580
Qy	2581	ACCAAGGATGCCCATACAGTACTCCACTATAGCAATTTCTTCCGAGAGTGTGTGC	2640
Db	2581	ACCAAGGATGCCCATACAGTACTCCACTATAGCAATTTCTTCCGAGAGTGTGTGC	2640
Qy	2641	TCTGGGGGCGCTTGCATCATATATATGTGATGAGTGCACATCACTGACACCACT	2700
Db	2641	TCTGGGGGCGCTTGCATCATATATATGTGATGAGTGCACATCACTGACACCACT	2700
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Db	4981	GGTGTGAGAGTACGTGAGAGTTACGGGGTGGGGATTTCCACATACGTGAGGGGCATG	5040
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Db	5101	GATGGGTGCGGTTCCACAGGTACGGCTCAGCGTGCAAACCCCTCTCTACGGAGAGAGTC	5160
QY	5161	ACATTCCGGGTGGGCTCAATCAATACCTGGTTGGGTACAGCTCCCATCGAGCCGAA	5220
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QY	5281	GCTAACCGTAAGCTGGCCAGGGGATCTCCCCCTCTGGGCGACACTATACGTAGACG	5340
Db	5281	GCTAACCGTAAGCTGGCCAGGGGATCTCCCCCTCTGGGCGACACTATACGTAGACG	5340
QY	5341	CTGTGCGCCCTCTCTTGAGGCAACATGCACCTCCATGACTCCCGGACGCTGAC	5400
Db	5341	CTGTGCGCCCTCTCTTGAGGCAACATGCACCTCCATGACTCCCGGACGCTGAC	5400
QY	5401	CTCATGAGGCCAACCTCTGTGTGGGGGAGAGATGGGCGGGGAATCACCCCGTGGAG	5460
Db	5401	CTCATGAGGCCAACCTCTGTGTGGGGGAGAGATGGGCGGGGAATCACCCCGTGGAG	5460
QY	5461	TCGAAATAAGTATGATATTTTGGACTCTTTGAGCCGCTCCAAAGCGAGAGATGAG	5520
Db	5461	TCGAAATAAGTATGATATTTTGGACTCTTTGAGCCGCTCCAAAGCGAGAGATGAG	5520
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QY	5881	TCTCCATGCCCCCTTGAGGGGAGCCGGGGATCCCGATCTCAGCGAGGCTCTTG	5940
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LOCUS AX036254
DEFINITION Sequence 3 from Patent EP1043399.
ACCESSION AX036254
VERSION AX036254.1 GI:11225870
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
REFERENCE 1 (bases 1 to 8001)
AUTHORS Bartschlag, R.D.
TITLE Hepatitis C virus cell culture system

JOURNAL Patent: EP 1043399-A 3 11-OCT-2000;
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Query Match 99.8%; Score 7960.6; DB 6; Length 8001;
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Db 541 TTGTCAAGACGACCTGTGCGGTGCTGAATGAATCTGACAGAGAGGCAAGCGGCTAT 600
Qy 589 CGTGGCTGGCCAGAGCGGGCTTCTTGGCGAGCTGTGCTGAGAGTGTACTGAAGCGG 648
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Qy 601 CGTGGCTGGCCAGAGCGGGCTTCTTGGCGAGCTGTGCTGAGAGTGTACTGAAGCGG 660
Db 601 CGTGGCTGGCCAGAGCGGGCTTCTTGGCGAGCTGTGCTGAGAGTGTACTGAAGCGG 660
Qy 649 GAAGGAGCTGTGCTATTTGGGCGAAGTCCGGGGCGAGATCTCTCTGATCTCACCTTG 708
Db 649 GAAGGAGCTGTGCTATTTGGGCGAAGTCCGGGGCGAGATCTCTCTGATCTCACCTTG 708
Qy 709 CTTCCTGCGAGAAATATCATCATGCTGATGATGCAATGCGGCGCTCATACCTTGATC 768
Db 709 CTTCCTGCGAGAAATATCATCATGCTGATGATGCAATGCGGCGCTCATACCTTGATC 768
Qy 721 CTTCCTGCGAGAAATATCATCATGCTGATGATGCAATGCGGCGCTCATACCTTGATC 780
Db 721 CTTCCTGCGAGAAATATCATCATGCTGATGATGCAATGCGGCGCTCATACCTTGATC 780
Qy 769 CGGCTACCTGCCCATTTGACACCAAGGAAACATGCGATGAGAGAGCACTACTGGA 828
Db 769 CGGCTACCTGCCCATTTGACACCAAGGAAACATGCGATGAGAGAGCACTACTGGA 828
Qy 781 CGGCTACCTGCCCATTTGACACCAAGGAAACATGCGATGAGAGAGCACTACTGGA 840
Db 781 CGGCTACCTGCCCATTTGACACCAAGGAAACATGCGATGAGAGAGCACTACTGGA 840
Qy 829 TGGAGCCGGCTTGTGATGATGATGTGAGAGAGAGACATCAGAGGCTCGCGCAG 888
Db 829 TGGAGCCGGCTTGTGATGATGATGTGAGAGAGAGACATCAGAGGCTCGCGCAG 888
Qy 841 TGGAGCCGGCTTGTGATGATGATGTGAGAGAGAGACATCAGAGGCTCGCGCAG 900
Db 841 TGGAGCCGGCTTGTGATGATGATGTGAGAGAGAGACATCAGAGGCTCGCGCAG 900

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QY	889	CCGAACTGTTGGCAGAGCTCAAGGGCGGCGATGCCGAGCGGAGAGATCGTGTACCC	948
Db	901	CCGAACGTGTTGGCCAGAGCTCAAGGGCGGCGATGCCGAGCGGAGAGATCGTGTACCC	960
QY	949	ATGGCATGCGTCTGTGGCGAATATCATGTGTGAAATAGCCGCTTTCTTGATTCATCG	1008
Db	961	ATGGCATGCGTCTGTGGCGAATATCATGTGTGAAATAGCCGCTTTCTTGATTCATCG	1020
QY	1009	ACTGTGCGCGGTGSGTGTGCGGAACCGCTATCAGACATAGCGTTGGCTTACCGGTATA	1068
Db	1021	ACTGTGCGCGGTGSGTGTGCGGAACCGCTATCAGACATAGCGTTGGCTTACCGGTATA	1080
QY	1069	TTGCTGAAGAGCTTGGCGGCGAATGGGGCGAACCGCTTCCTGTGTTTACGGATATGCGG	1128
Db	1081	TTGCTGAAGAGCTTGGCGGCGAATGGGGCGAACCGCTTCCTGTGTTTACGGATATGCGG	1140
QY	1129	CTCCGATTCGACAGCGCATCGCCTTCTATCGCCTTCTTGAAGAGTCTTCTGAGTTTAA	1188
Db	1141	CTCCGATTCGACAGCGCATCGCCTTCTATCGCCTTCTTGAAGAGTCTTCTGAGTTTAA	1200
QY	1189	CAGACCAACAGSGTTCCCTCTAGGCGGATCAATTGCGCCCTCTCCCTCCCGCCGCT	1248
Db	1201	CAGACCAACAGSGTTCCCTCTAGGCGGATCAATTGCGCCCTCTCCCTCCCGCCGCT	1260
QY	1249	AAGTTCCTGGCCGAAGCGGTGTGAAATAGCCGCGTGGCTTGGTTCATATATTTATTT	1308
Db	1261	AAGTTCCTGGCCGAAGCGGTGTGAAATAGCCGCGTGGCTTGGTTCATATATTTATTT	1320
QY	1309	TCCACCATATTCGCTCTTTTGGCAATGTGAGGGCCGGAAACCTGGCCCTGTCTTCTG	1368
Db	1321	TCCACCATATTCGCTCTTTTGGCAATGTGAGGGCCGGAAACCTGGCCCTGTCTTCTG	1380
QY	1369	ACGAGCTTCCTTGGGGGTCTTTTCCCTCTCGCCAAAGGATGCAAGTCTTTGAATGTC	1428
Db	1381	ACGAGCTTCCTTGGGGGTCTTTTCCCTCTCGCCAAAGGATGCAAGTCTTTGAATGTC	1440
QY	1429	GTCGAAGAGCAAGTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTGAGCAACCTT	1488
Db	1441	GTCGAAGAGCAAGTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTGAGCAACCTT	1500
QY	1489	TGCGAGCAGGGGGAACCCCGCACTGGCGAGAGTGCTCTGGGCGCAAAACGCAAGGTGA	1548
Db	1501	TGCGAGCAGGGGGAACCCCGCACTGGCGAGAGTGCTCTGGGCGCAAAACGCAAGGTGA	1560
QY	1549	TAAATATACACCTGCAAAAGGGGCGACACACCCAGTGCCAGTGTGAGTTGATAGTTGTG	1608
Db	1561	TAAATATACACCTGCAAAAGGGGCGACACACCCAGTGCCAGTGTGAGTTGATAGTTGTG	1620
QY	1609	GAAAGAGTCAAAATGCTCTCTTAACCGTATTCACAGAGGGCTTAAGATATGCCAGAG	1668
Db	1621	GAAAGAGTCAAAATGCTCTCTTAACCGTATTCACAAAGGGCTTAAGATATGCCAGAG	1680
QY	1669	GTACCCCATTTGTGGAGTATGATCTGGGGGCGCTCGGTGCACATGCTTTACAATGTTTATG	1728
Db	1681	GTACCCCATTTGTGGAGTATGATCTGGGGGCGCTCGGTGCACATGCTTTACAATGTTTATG	1740
QY	1729	TCGAGGTTAAAAAAGCTGTAGGCCCCCGGACACAGGGGAGCTGTCTTCTTTGAAAAA	1788
Db	1741	TCGAGGTTAAAAAAGCTGTAGGCCCCCGGACACAGGGGAGCTGTCTTCTTTGAAAAA	1800
QY	1789	CAGATATATACAGTGGGCTATTAGGGCTTATCCCAACAGCGAGAGGCTTACTTGGC	1848
Db	1801	CAGATATATACAGTGGGCTATTAGGGCTTATCCCAACAGCGAGAGGCTTACTTGGC	1860
QY	1849	TGCATCATCACTAGCCTCACAGGCGCGGAGACAGGACCAAGTCAAGGGGAGGTCCAGGTG	1908
Db	1861	TGCATCATCACTAGCCTCACAGGCGCGGAGACAGGAAACAAGTCAAGGGGAGGTCCCAAGT	1920
QY	1909	GTCGCCACCGGAACAAATTTTCTGAGGAGCTGTGTCGAAGGGGTGTGTGACATGTC	1968
Db	1921	GTCGCCACCGGAACAAATTTTCTCTGAGGAGCTGTGTCGAAGGGGTGTGTGACATGTC	1980
QY	1969	TATATGGTGGCGGCTTAAAGACCTTGGCGGCGCCAAAGGGCCATCAACCCCAATGTAC	2028

Db	1981	TATCATGTGTCGGGCTCAAAGACCTTTCGGGCCCAAGGGCCCAATATCCCAATATGAC	2040
Qy	2029	ACCAATGTGAGACAGACCTGTGAGGTGCGANAGCGCCCCGGGGGCGCTTCCTTGACA	2088
Db	2041	ACCAATGTGAGACAGACCTGTGAGGTGCGANAGCGCCCCGGGGGCGCTTCCTTGACA	2100
Qy	2089	CCATGCACCTGGGGGAGCTCGGACCTTACTGGTCAACGAGGATGCGATGCTACTTCGG	2148
Db	2101	CCATGCACCTGGGGGAGCTCGGACCTTACTGGTCAACGAGGATGCGATGCTACTTCGG	2160
Qy	2149	GTCGCGCGGCGGGGAGACAGAGGGGGAGGACTACTGCCCCAGGCGCCCTCCTACTTG	2208
Db	2161	GTCGCGCGGCGGGGAGACAGAGGGGGAGGACTACTGCCCCAGGCGCCCTCCTACTTG	2220
Qy	2209	AAGGCGCTTTCGGGGGGTCCACTGCTCTGGCCCTCGGGGAGCCCTGTGGGACTCTTGG	2268
Db	2221	AAGGCGCTTTCGGGGGGTCCACTGCTGTCGCCCTCGGGGAGCCTGTGGGACTCTTGG	2280
Qy	2269	GTCGCGGTGACACCGAGGGGTTTCGAGAGCGGTGAGCTTTGTACCCCTCAGTCTATG	2328
Db	2281	GTCGCGGTGACACCGAGGGGTTTCGAGAGCGGTGAGCTTTGTACCCCTCAGTCTATG	2340
Qy	2329	GAACACACTATGCGGTCCCCGGTCTTCAAGSACACTCGTCCCTCGCGCTACCAGAG	2388
Db	2341	GAACACACTATGCGGTCCCCGGTCTTCAAGSACACTCGTCCCTCGCGCTACCAGAG	2400
Qy	2389	ACATTCAGGTGGCCCATCTACAGCCCCCTACTGTTAGCGGGAAGAGACTAAGTGGCG	2448
Db	2401	ACATTCAGGTGGCCCATCTACAGCCCCCTACTGTTAGCGGGAAGAGACTAAGTGGCG	2460
Qy	2449	GCTGCGTATGCACGCCAAGGGTATAAAGTGCTTGTCTGAACCCGTGCGCGCCGACAC	2508
Db	2461	GCTGCGTATGCACGCCAAGGGTATAAAGTGCTTGTCTGAACCCGTGCGCGCCGACAC	2520
Qy	2509	CTAGGTTTGGGGGCGTATATGTCTAAGGACATGTTGTGACCTTAACATGANAAGCGGG	2568
Db	2521	CTAGGTTTGGGGGCGTATATGTCTAAGGACATGTTGTGACCTTAACATGANAAGCGGG	2580
Qy	2569	GTAAGACACTACACACGGGGTCCCCCATCAGTACCTCCACTATGGAAGTTTCTGGC	2628
Db	2581	GTAAGACACTACACACGGGGTCCCCCATCAGTACCTCCACTATGGAAGTTTCTGGC	2640
Qy	2629	GAGCGTGTGCTCTGTGGGGCGCCTATACATCATATATGTATGTATGGTCCACTCAAT	2688
Db	2641	GAGCGTGTGCTCTGTGGGGCGCCTATACATCATATATGTATGTATGGTCCACTCAAT	2700
Qy	2689	GACTCGACACTATCTCTGGGACATCGGACACTCTGTGACAAACGGAGAGCGGTGAGCG	2748
Db	2701	GACTCGACACTATCTCTGGGACATCGGACACTCTGTGACAAACGGAGAGCGGTGAGCG	2760
Qy	2749	CGACTGTGTGCTGTGCCACCGCTACGCTCCGGATCGGTCACTGCGCATCCAAAC	2808
Db	2761	CGACTGTGTGCTGTGCCACCGCTACGCTCCGGATCGGTCACTGCGCATCCAAAC	2820
Qy	2809	ATCAGAGAGGTGGCTGTGTCCAGCACTGAGAAATCCCTTTATGGCAAGGCATCCCC	2868
Db	2821	ATCAGAGAGGTGGCTGTGTCCAGCACTGAGAAATCCCTTTATGGCAAGGCATCCCC	2880
Qy	2869	ATCAGAGCACTACAAGGGGGGAGGACCTCATTTTCTGCATTCCAGAAAGAAATGTAT	2928
Db	2881	ATCAGAGCACTACAAGGGGGGAGGACCTCATTTTCTGCATTCCAGAAAGAAATGTAT	2940
Qy	2929	GAGTCGCCCGCGAAGCTGTGTCCCGCCCGGACATGCTGTAGCATATTCACGGGCGCT	2988
Db	2941	GAGTCGCCCGCGAAGCTGTGTCCCGCCCGGACATGCTGTAGCATATTCACGGGCGCT	3000
Qy	2989	GATGTATCCGCTCATACCACACTAGCGGAGCGTCAATTTGTCGTAGCAACGAGCGCTTAATG	3048
Db	3001	GATGTATCCGCTCATACCACACTAGCGGAGCGTCAATTTGTCGTAGCAACGAGCGCTTAATG	3060
Qy	3049	ACGGGCTTTACCGGCAATTTGCATCTAGTATGCATGTCAATATATGTGTACCCAGACA	3108

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DB 3121 GTGCACTTCAGCTGGAGCCCGACCTTCACCATTTGAGACGACGACCGGTCACAGAGCGG 3180
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DB 3181 GTGTACGCTCGACAGCGGCGAGGAGAGTGTAGGGGACAGATTACAGGTTT 3240
QY 3229 GTGATCCAGGAGAACGGCCCTGCGGATGTGATTCCTCGGTTCTGTCGCGAGTCTAT 3288
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QY 3469 AACCTCCCTTACCTGTGATGATACAGAGCTACGCTGTGCGCAGGCTCAGGCTCCACT 3528
DB 3481 AACCTCCCTTACCTGTGATGATACAGAGCTACGCTGTGCGCAGGCTCAGGCTCCACT 3540
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DB 3661 ACCAATACATCATGATGATGATGCGGCTACCTGGAGTGTGACAGACACCTGGATG 3720
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DEFINITION			
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ACCESSION			
VERSION			
KEYWORDS			
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ORGANISM			Hepatitis C virus
REFERENCE			Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepadnavirus. 1 (bases 1 to 8001)

AUTHORS Bartenschlager R.D.
TITLE Hepatitis C virus cell culture system
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FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.4%; Score 7943; DB 6; Length 8001;
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OY 181 GACGACCGGGGCTCTTCTTGATCAACCCGCTCATGCTGAGATTTGGCGCTGCCCC 240
Db 181 GACGACCGGGGCTCTTCTTGATCAACCCGCTCATGCTGAGATTTGGCGCTGCCCC 240
OY 241 GCGGACTCGTAGCGGAGTAGTGTGTTGGTGGCCAAAGGCTTGTGACTGCTGTATAG 300
Db 241 GCGGACTCGTAGCGGAGTAGTGTGTTGGTGGCCAAAGGCTTGTGACTGCTGTATAG 300
OY 301 GTGCTTGGAGTGCCTCCGGGAGAGTCTGTAGACCGTGCACACATGACAGAACTCTTAAC 360
Db 301 GTGCTTGGAGTGCCTCCGGGAGAGTCTGTAGACCGTGCACACATGACAGAACTCTTAAC 360
OY 361 CTCAAAGAAAACCAA-----GGGGCGCCATGATTGAACAAGATGGATTGC 408
Db 361 CTCAAAGAAAACCAAAGTAAACAACGAGGCGCCCATGATTGAACAAGATGGATTGC 408
OY 409 ACGAGAGTTCGCCGCGCTTGGGTGAGAGGCTATTCGCTATGACTGGGCACACAGA 468
Db 409 ACGAGAGTTCGCCGCGCTTGGGTGAGAGGCTATTCGCTATGACTGGGCACACAGA 468
OY 421 ACGGAGGTTCTCCGGCGCTTGGGTGAGAGGCTATTCGCTATGACTGGGCACACAGA 480
Db 421 ACGGAGGTTCTCCGGCGCTTGGGTGAGAGGCTATTCGCTATGACTGGGCACACAGA 480
OY 469 CAATGGCTGCTGTGATGCGCGCTGTTCGGGCTGTACGCGAGGGGCGCCGGTCTTT 528
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OY 481 CAATCGGCTGCTGTGATGCGCGCTGTTCGGGCTGTACGCGAGGGGCGCCGGTCTTT 540
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OY 529 TTGTCAAGACGAGCTGTGCGGCTGCTGATGATGACGAGGAGGAGCGACCGGCTAT 588
Db 529 TTGTCAAGACGAGCTGTGCGGCTGCTGATGATGACGAGGAGGAGCGACCGGCTAT 588
OY 541 TTGTCAAGACGAGCTGTGCGGCTGCTGATGATGACGAGGAGGAGCGACCGGCTAT 600
Db 541 TTGTCAAGACGAGCTGTGCGGCTGCTGATGATGACGAGGAGGAGCGACCGGCTAT 600
OY 589 CGTGGCTGGCAGACGAGGCGCTTCTTGGCGAGCTGTGCTGACGTTTGACTGAAGCG 648
Db 589 CGTGGCTGGCAGACGAGGCGCTTCTTGGCGAGCTGTGCTGACGTTTGACTGAAGCG 648
OY 601 CGTGGCTGGCAGACGAGGCGCTTCTTGGCGAGCTGTGCTGACGTTTGACTGAAGCG 660
Db 601 CGTGGCTGGCAGACGAGGCGCTTCTTGGCGAGCTGTGCTGACGTTTGACTGAAGCG 660
OY 649 GAAAGGATAGGCTGTATGGGAGAGTGGCGGGGAGAGTCTGCTGATCTCCACTTG 708
Db 649 GAAAGGATAGGCTGTATGGGAGAGTGGCGGGGAGAGTCTGCTGATCTCCACTTG 708
OY 661 GAAAGGATAGGCTGTATGGGAGAGTGGCGGGGAGAGTCTGCTGATCTCCACTTG 720
Db 661 GAAAGGATAGGCTGTATGGGAGAGTGGCGGGGAGAGTCTGCTGATCTCCACTTG 720
OY 709 CTCCTGCCAGAAAGTATCATGCTGCTGATGCTGATGCTGCGCGCTGCATACGCTTGATC 768
Db 709 CTCCTGCCAGAAAGTATCATGCTGCTGATGCTGATGCTGCGCGCTGCATACGCTTGATC 768
OY 721 CTCCTGCCAGAAAGTATCATGCTGCTGATGCTGATGCTGCGCGCTGCATACGCTTGATC 780
Db 721 CTCCTGCCAGAAAGTATCATGCTGCTGATGCTGATGCTGCGCGCTGCATACGCTTGATC 780
OY 769 CGGCTACTGCGCATTCGACACCAAGCAAACTCGCATCGAGGAGCAAGTAACTCGGA 828
Db 769 CGGCTACTGCGCATTCGACACCAAGCAAACTCGCATCGAGGAGCAAGTAACTCGGA 828
OY 781 CGGCTACTGCGCATTCGACACCAAGCAAACTCGCATCGAGGAGCAAGTAACTCGGA 840
Db 781 CGGCTACTGCGCATTCGACACCAAGCAAACTCGCATCGAGGAGCAAGTAACTCGGA 840
OY 829 TGAAGCGGCTCTGTGATGAGATGATGAGCAAGAGCATCAGGGGCTGCGCCAG 888
Db 829 TGAAGCGGCTCTGTGATGAGATGATGAGCAAGAGCATCAGGGGCTGCGCCAG 888
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Db 841 TGAAGCGGCTCTGTGATGAGATGATGAGCAAGAGCATCAGGGGCTGCGCCAG 900
OY 889 CCGAAGCTTTTCGCGAGCTCAAGGCGCGCATGCGCCGACGGCGAGTCTGCTGAGACCC 948
Db 901 CCGAAGCTTTTCGCGAGCTCAAGGCGCGCATGCGCCGACGGCGAGTCTGCTGAGACCC 960
OY 949 ATGAGCATGCTGCTTCCGCAATATCATGCTGAGAAATGCGCCCTTTCTGATTCATCG 1008
Db 961 ATGAGCATGCTGCTTCCGCAATATCATGCTGAGAAATGCGCCCTTTCTGATTCATCG 1020
OY 1009 ACTGTGCGCGCTGTGGTGTGGGAGCGGCTATCAGAGCATAGCGTTGGCTACCCGCTGATA 1068
Db 1021 ACTGTGCGCGCTGTGGTGTGGGAGCGGCTATCAGAGCATAGCGTTGGCTACCCGCTGATA 1080
OY 1069 TTGCTGAAGAGCTGTGGGCGGAATGAGGCTGACCGCTTCTGCTGCTTACGATGCGCG 1128
Db 1081 TTGCTGAAGAGCTGTGGGCGGAATGAGGCTGACCGCTTCTGCTGCTTACGATGCGCG 1140
OY 1129 CTCGCGATTCGACGCGCATGCGCTTCTATGCGCTTCTTGACAGATTCTTGTAGTTTAA 1188
Db 1141 CTCGCGATTCGACGCGCATGCGCTTCTATGCGCTTCTTGACAGATTCTTGTAGTTTAA 1200
OY 1189 CAGACCAAGAGTTTCCCTCTAGCGGATCAATTCGAGCCCTTCCCTCCCGCCCT 1248
Db 1201 CAGACCAAGAGTTTCCCTCTAGCGGATCAATTCGAGCCCTTCCCTCCCGCCCT 1260
OY 1249 AACGTTACTGCGCAGACCCCTTGGAATTAAGCCCGGTGCTGTTGTTCTATATGTTATT 1308
Db 1261 AACGTTACTGCGCAGACCCCTTGGAATTAAGCCCGGTGCTGTTGTTCTATATGTTATT 1320
OY 1309 TCCACCATATGCGGCTTTTGGCAATGTAGAGGCGCGGAACCTGAGCCCTGCTCTTG 1368
Db 1321 TCCACCATATGCGGCTTTTGGCAATGTAGAGGCGCGGAACCTGAGCCCTGCTCTTG 1380
OY 1369 ACGAGCATTCCTAGGGGCTCTTCCCTCTGCGCAAGAGATGCAAGGCTGTTGAATTGC 1428
Db 1381 ACGAGCATTCCTAGGGGCTCTTCCCTCTGCGCAAGAGATGCAAGGCTGTTGAATTGC 1440
OY 1429 GTGAAGGAGAGTTCCTCTGGAAGCTTCTTGAAGCAAAACAGTCTGTAGAGGACCTT 1488
Db 1441 GTGAAGGAGAGTTCCTCTGGAAGCTTCTTGAAGCAAAACAGTCTGTAGAGGACCTT 1500
OY 1489 TGCAGGACGCGGAACCCCGACCTGCGAGAGGTGCTTGCAGGCGCAAAACCCAGCTGTA 1548
Db 1501 TGCAGGACGCGGAACCCCGACCTGCGAGAGGTGCTTGCAGGCGCAAAACCCAGCTGTA 1560
OY 1549 TAAATATACCTGCAAGAGCGGCGACACCCAGTGCACCTGTGTGATGATGATGTTG 1608
Db 1561 TAAATATACCTGCAAGAGCGGCGACACCCAGTGCACCTGTGTGATGATGATGTTG 1620
OY 1609 GAAAGAGTCAATATGCTCTCTCAAGCGTATTTACAAGGGGCTGGAAGATGCCCAAG 1668
Db 1621 GAAAGAGTCAATATGCTCTCTCAAGCGTATTTACAAGGGGCTGGAAGATGCCCAAG 1680
OY 1669 GTACCCCTTTGTATGGGATCTGATCTGGGCGCTGGGTGCAATGCTTTTACATGTTTAC 1728
Db 1681 GTACCCCTTTGTATGGGATCTGATCTGGGCGCTGGGTGCAATGCTTTTACATGTTTAC 1740
OY 1729 TCGAGTTAAAAAAGCTGTAGGCGCCCGGAGAACAGGGGAGCTGTTCCTTTGAAAAA 1788
Db 1741 TCGAGTTAAAAAAGCTGTAGGCGCCCGGAGAACAGGGGAGCTGTTCCTTTGAAAAA 1800
OY 1789 CACGATTAATACATGCGGCTATTAGCGGCTACTTCCAAAGACGCGAGGCTACTTTGGC 1848
Db 1801 CACGATTAATACATGCGGCTATTAGCGGCTACTTCCAAAGACGCGAGGCTACTTTGGC 1860
OY 1849 TGCATCATCACTAGCTTACAGGCGCGGAGACAGAAACAGGTGCAAGGGGAGGCTCAAGT 1908
Db 1861 TGCATCATCACTAGCTTACAGGCGCGGAGACAGAAACAGGTGCAAGGGGAGGCTCAAGT 1920
OY 1909 GTCTTCACCGGACACAAATCTTCTGTGGAGCTGCTGCTCAATGCGCTGTGTGACTGTC 1968
Db 1921 GTCTTCACCGGACACAAATCTTCTGTGGAGCTGCTGCTCAATGCGCTGTGTGACTGTC 1980
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QY	1969	TATATATGTCGGGCTCTCAAGAACCTTCGCCGGCCCAAGAGGCCCATATACCCAAATGTAC	2028
Db	1981	TATATATGTCGGGCTCTCAAGAACCTTCGCCGGCCCAAGAGGCCCATATACCCAAATGTAC	2040
QY	2029	ACCAATGTGACAGAGACACCTGTCGGCTGGACAGGCCGCCCGGGAGGCCGTTCTTGACA	2088
Db	2041	ACCAATGTGACAGAGACACCTGTCGGCTGGACAGGCCGCCCGGGAGGCCGTTCTTGACA	2100
QY	2089	CCATGCACTGCGGGCACTTGGACCTTTACTTGTGTACAGAGCATGCCGATGTCAATTCG	2148
Db	2101	CCATGCACTGCGGGCACTTGGACCTTTACTTGTGTACAGAGCATGCCGATGTCAATTCG	2160
QY	2149	GTGGCGCGGGGGGCGACACAGAGGGGAGACCTTACTTCCCCAGGCCCGTCTCCACTTG	2208
Db	2161	GTGGCGCGGGGGGCGACACAGAGGGGAGACCTTACTTCCCCAGGCCCGTCTCCACTTG	2220
QY	2209	AAGGGCTCTTCGGGCGGTCCACTGCTCTGCCCTGGGGCACGCTGTGGCATCTTCG	2268
Db	2221	AAGGGCTCTTCGGGCGGTCCACTGCTCTGCCCTGGGGCACGCTGTGGCATCTTCG	2280
QY	2269	GCTCCCTGTGACACCCGAGGGGTTGGGAAGGGCGGTGAATTTGTACCCGTGAGCTATG	2328
Db	2281	GCTCCCTGTGACACCCGAGGGGTTGGGAAGGGCGGTGAATTTGTACCCGTGAGCTATG	2340
QY	2329	GAAAACCACTATGGGTCCTCCCGGTCTTACGGCACTCGTCCCTCCGGCGATACCGAG	2388
Db	2341	GAAAACCACTATGGGTCCTCCCGGTCTTACGGCACTCGTCCCTCCGGCGATACCGAG	2400
QY	2389	ACATTCAGAGGGGCGCCATCTACAGGCCCTACGTGTAGGGGAAGAGCACTTAAGTTGCG	2448
Db	2401	ACATTCAGAGGGGCGCCATCTACAGGCCCTACGTGTAGGGGAAGAGCACTTAAGTTGCG	2460
QY	2449	GCTGCGTATGCAAGCCAAAGGATATAAGGTGTGTCTGTAACCCGTCGTGCGCCGAC	2508
Db	2461	GCTGCGTATGCAAGCCAAAGGATATAAGGTGTGTCTGTAACCCGTCGTGCGCCGAC	2520
QY	2509	CTAGGTTCCGGGGGTATATGTCTAAGGGCAGTGTATGAGCCCTAACATCGAAGCGGG	2568
Db	2521	CTAGGTTCCGGGGGTATATGTCTAAGGGCAGTGTATGAGCCCTAACATCGAAGCGGG	2580
QY	2569	GTAAGGACCATCACACGGGTGCCCCATCACGTACTCCACCTATGGCAAGTTCTTGGC	2628
Db	2581	GTAAGGACCATCACACGGGTGCCCCATCACGTACTCCACCTATGGCAAGTTCTTGGC	2640
QY	2629	GACGGTGGTTGCTCTGGGGGCGGCTATGACATATATATGTGATGAGTGGCCACTCACT	2688
Db	2641	GACGGTGGTTGCTCTGGGGGCGGCTATGACATATATATGTGATGAGTGGCCACTCACT	2700
QY	2689	GACTCGACCACTATCTTGGGCATTCGGCACAGTCTTGAGCAAGCGGAGCGGTGGACG	2748
Db	2701	GACTCGACCACTATCTTGGGCATTCGGCACAGTCTTGAGCAAGCGGAGCGGTGGACG	2760
QY	2749	CGACTCGTGTGTCTGCGCACCGGTACGGCCCTCGGGATGCGTACCGTGCACATCAAC	2808
Db	2761	CGACTCGTGTGTCTGCGCACCGGTACGGCCCTCGGGATGCGTACCGTGCACATCAAC	2820
QY	2809	ATCGAGGAGGTGCTCTGTCCAGACTGAGAAATCCCTTTATATGGCAAGCCATCC	2868
Db	2821	ATCGAGGAGGTGCTCTGTCCAGACTGAGAAATCCCTTTATATGGCAAGCCATCC	2880
QY	2869	ATCGAGGACATCAAGGGGGGAGGAGCACTATTTCTGCAATTCGAAGAAAGATGTAT	2928
Db	2881	ATCGAGGACATCAAGGGGGGAGGAGCACTATTTCTGCAATTCGAAGAAAGATGTAT	2940
QY	2929	GAGCTCGCGCGGAGAGCTGTCCGCTTCGCACTCAATGCTGTAGCATATTAACGGGGCCTT	2988
Db	2941	GAGCTCGCGCGGAGAGCTGTCCGCTTCGCACTCAATGCTGTAGCATATTAACGGGGCCTT	3000
QY	2989	GATGTATCCGTCATACCAACTAGCGGAGAGCTATGTGTGTAGCAAGSAGCCTCTAATG	3048
Db	3001	GATGTATCCGTCATACCAACTAGCGGAGAGCTATGTGTGTAGCAAGSAGCCTCTAATG	3060

Qy	3049	ACGGCTTTTACCGGGCAATTTTCAGACTAGATGACGACTGCAATACATATGTGTACCCAGACA	3108
Db	3061	ACGGGCTTTACGGCTGTGCTTCAGCTACGATGACGATGACTGCATATGCTATGCTACCCAGACA	3120
Qy	3109	GTGCACTTCACCGCTGGAACCCGACCTTTCACCATTTGAAGACGACGACCGTGCACAAAGACGC	3168
Db	3121	GTGCACTTCACCGCTGGAACCCGACCTTTCACCATTTGAAGACGACGACCGTGCACAAAGACGC	3180
Qy	3169	GTGTACAGCTTGGCAGCGGAGGACGAGACAGCTGGGTAGGGGAGGATGGGATTTACAGGTTT	3228
Db	3181	GTGTACAGCTTGGCAGCGGAGGACGAGACAGCTGGGTAGGGGAGGATGGGATTTACAGGTTT	3240
Qy	3229	GTGACTCCAGAGAACGCGCCCTGGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTCTAT	3288
Db	3241	GTGACTCCAGAGAACGCGCCCTGGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTCTAT	3300
Qy	3289	GACGGGGGCTGTGGTTTGTGTGACGTCACGCCCCCGGACAGCTCAAGTTAGTTGGGGCT	3348
Db	3301	GACGGGGGCTGTGGTTTGTGTGACGTCACGCCCCCGGACAGCTCAAGTTAGTTGGGGCT	3360
Qy	3349	TACCTAAACACACGAGGGTTGCCGTGTGCACGAGACCATCTGGAAGTTCTGGACAGGCTC	3408
Db	3361	TACCTAAACACACGAGGGTTGCCGTGTGCACGAGACCATCTGGAAGTTCTGGAGAGGCTC	3420
Qy	3409	TTTACAGGCTTCACCCCATATAGAGCCCATTTTGTTCACAGCTAAGAGGACAGAGAC	3468
Db	3421	TTTACAGGCTTCACCCCATATAGAGCCCATTTTGTTCACAGCTAAGAGGACAGAGAC	3480
Qy	3469	AACTTCCCTACCTGATAGCATACCAAGCTACGGTGTGCGGACGAGGCTCAGGCTCACCT	3528
Db	3481	AACTTCCCTACCTGATAGCATACCAAGCTACGGTGTGCGGACGAGGCTCAGGCTCACCT	3540
Qy	3529	CCATGTGGGACCAAAATGTGGAAGTGTCTATACGCTAAAGCCTACGCTGACGGGACA	3588
Db	3541	CCATGTGGGACCAAAATGTGGAAGTGTCTATACGCTAAAGCCTACGCTGACGGGACA	3600
Qy	3589	ACGCCCCGTGTATAGGCTTGGAGCCGTTCAAACGAGGTTACTACACACCCCATTA	3648
Db	3601	ACGCCCCGTGTATAGGCTTGGAGCCGTTCAAACGAGGTTACTACACACCCCATTA	3660
Qy	3649	ACCAATATCATCATAGGATGATGATGCGCTGACCTGGAGGTGTGTACAGGACCTGGGAT	3708
Db	3661	ACCAATATCATCATAGGATGATGATGCGCTGACCTGGAGGTGTGTACAGGACCTGGGAT	3720
Qy	3709	CTGGTAGGCGGAGTCTTAGCAGAGCTGTGGCGGCTATTGGCTGACAAACAGCAGCGTGGCT	3768
Db	3721	CTGGTAGGCGGAGTCTTAGCAGAGCTGTGGCGGCTATTGGCTGACAAACAGCAGCGTGGCT	3780
Qy	3769	ATTGTGGGACAGATCATCTTGTGCGGAAGGCCCGGCATATTCCGACAGAGGAAGTCTT	3828
Db	3781	ATTGTGGGACAGATCATCTTGTGCGGAAGGCCCGGCATATTCCGACAGAGGAAGTCTT	3840
Qy	3829	TACCGGGAGTCTGATGAGATGGAAGAGTGGCGCTCACACTCCCTAACATCGAANAAGGA	3888
Db	3841	TACCGGGAGTCTGATGAGATGGAAGAGTGGCGCTCACACTCCCTAACATCGAANAAGGA	3900
Qy	3889	ATGCAAGCTCGCGCAACAATTCAAACAGAAAGCAATCGGGTCTGTGCAACAGCCACCAAG	3948
Db	3901	ATGCAAGCTCGCGCAACAATTCAAACAGAAAGCAATCGGGTCTGTGCAACAGCCACCAAG	3960
Qy	3949	CAAGGAGAGGCTGTGCTGCCCGGTGGTGGATTCGAATGGGCGGACCCCTGCAACCTTTGG	4008
Db	3961	CAAGGAGAGGCTGTGCTGCCCGGTGGTGGATTCGAATGGGCGGACCCCTTCTGG	4020
Qy	4009	GGGAAGCATATGTGGAAATTTTCATCAGCGGATACAAATATTTAGCAGGCTTGTCACTTG	4066
Db	4021	GGGAAGCATATGTGGAAATTTTCATCAGCGGATACAAATATTTAGCAGGCTTGTCACTTG	4080
Qy	4069	CGTGGCAACCCCGGAGTATGAGATCATGCTATGTGGCAATTCACAGCCCTATACAGCCGCTG	4128
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Qy	4129	ACCAACCAACATACCTCTGTGTTTAACTACCTTGGGGAGATGGGTGGCGCCCACTTGCT	4188

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Db 4381 CTACTCCCTGCTATCTCTCTCTGCGCCCTAGTGTGCGGCTCGTGTGCGCAGAT 4440
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Oy 4609 CAGTGCATCAACGAGGACTGCTCCACGCCATGCTCCGGCTGTGGCTAAGAGATGTTTG 4668
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Db 6301 TATGGGGAAGAGAGCTCGGAGACTATCCAGCAAGGCGTTAACCCATCCGCTCGTG 6360
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QY 6349 TGGAAAGACTTGTCTGGAAGACACTGAGACACCAATTGACACACCATATGACGCAAAAAAT 6408
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LOCUS AX036257
DEFINITION Sequence 6 from Patent EP104339.
ACCESSION AX036257
VERSION AX036257.1 GI:11225873
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
REFERENCE 1 (bases 1 to 8001)
AUTHORS Bartenschlager, R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 6 11-OCT-2000;
BARTENSCHLAGER RALF DR (DE)
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BASE COUNT 1646 a 2372 c 2249 g 1734 t
ORIGIN

Query Match 99.4% Score 7941.4; DB 6; Length 8001;
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Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;

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Qy 5929 GACGGGCTCTGTCTACCGTAAGCGAGAGGCTAGTGAAGAGCTGTCTGTCTGATG 5988
Db 5941 GACGGGCTCTGTCTACCGTAAGCGAGAGGCTAGTGAAGAGCTGTCTGTCTGATG 6000
Qy 5989 TCTTACACATGAGACAGGCGCCCTGATACGCCCATGCGGCTGGCGAGGAACCAAGTGGCC 6048
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Qy 6109 CGCAGCCGAACCTGCGGCGAGGAAGTACTTTGACAGACTGAGAGTCCCTGGACGAC 6168
Db 6121 CGCAGCCGAACCTGCGGCGAGGAAGTACTTTGACAGACTGAGAGTCCCTGGACGAC 6180
Qy 6169 CACTACCGGAGCTGCTCAAGGAGATGAAGGCGAAGGCTGCCAGTAAAGTAAACTT 6228
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Qy 6229 CTATCCGTGAGAGAGCTGTAGAGCTGAGCCGCCACATTCGGCGAGATTAATTGGC 6288
Db 6241 CTATCCGTGAGAGAGCTGTAGAGCTGAGCCGCCACATTCGGCGAGATTAATTGGC 6300
Qy 6289 TATGGGCAAGAGAGAGCTCCGGAACCTTCCAGCAAGGCGTAAACATCCGCTCCGTG 6348
Db 6301 TATGGGCAAGAGAGAGCTCCGGAACCTTCCAGCAAGGCGTAAACATCCGCTCCGTG 6360
Qy 6349 TGAAGAGACTTGTGAAGACACTGAGACACCAATTGACACACATCATGCAAAAAAT 6408
Db 6361 TGAAGAGACTTGTGAAGACACTGAGACACCAATTGACACACATCATGCAAAAAAT 6420
Qy 6409 GAGTGTTCCTGCGTCCAAACGAGAGAGAGGGGGCGCAAGGCACTGCGCTTATGATTC 6468
Db 6421 GAGTGTTCCTGCGTCCAAACGAGAGAGAGGGGGCGCAAGGCACTGCGCTTATGATTC 6480
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Db 6481 CCAGATTTGGGGGTTCTGTGTGTGAGAAAAATGGCCCTTTAGATGTGATCTCCACCTTC 6540
Qy 6529 CCTCAGGCGGTGATGGGCTCTCTATAGATTTCCATACCTCTCTGAGACGGCGGTGAG 6588
Db 6541 CCTCAGGCGGTGATGGGCTCTCTATAGATTTCCATACCTCTCTGAGACGGCGGTGAG 6600
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Db 6601 TTCTGTGTAATGCTGCGTGAAGAGCAAGAAATGCTTAAGCTTGCATATGACACCGC 6660
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Qy	6649	TGTTTTAGCTCAACGGTCACTGAGAAATGACATCCGTTGTTGAGAGTCAATCTACCAATGT	6708
Db	6661	TGTTTTAGCTCAACGGTCACTGAGAAATGACATCCGTTGTTGAGAGTCAATCTACCAATGT	6720
Qy	6709	TGTGACTGGGGCCCCGAAGCCACACAGGGCAATAGGTGCTCTACAGAGGGGCTTACTC	6768
Db	6721	TGTGACTTGGGGCCCCGAAGCCACACAGGGCAATAGGTGCTCTACAGAGGGGCTTACTC	6780
Qy	6769	GGGGGGCCCCGACTAATTCTAAAGGGCAGAACTGCGCTATAGCCGGTGC CGCGAGC	6828
Db	6781	GGGGGGCCCCGACTAATTCTAAAGGGCAGAACTGCGCTATAGCCGGTGC CGCGAGC	6840
Qy	6829	GSTGACTGAGACACACTCGGTAATTAACCTACATGTTACTCTGAAGGCGCTCGGCG	6888
Db	6841	GSTGACTGAGACACACTCGGTAATTAACCTACATGTTACTCTGAAGGCGCTCGGCG	6900
Qy	6889	TGTGAGCTGCGAAGCTCCAGAGACTGCAAGTCTGTATGCGAGACAGCACTTGTGCT	6948
Db	6901	TGTGAGCTGCGAAGCTCCAGAGACTGCAAGTCTGTATGCGAGACAGCACTTGTGCT	6960
Qy	6949	ATCTGTGAACCGGGGGAGCCCAAGAGAGAGAGGAGCGCTACGGGCTTACAGGAGCT	7008
Db	6961	ATCTGTGAACCGGGGGAGCCCAAGAGAGAGAGGAGCGCTACGGGCTTACAGGAGCT	7020
Qy	7009	ATGACTAATTAATCTGCGCCCCCTGGGGAGCCGCCCAACACAGAAATACGATCTGGAGTTG	7068
Db	7021	ATGACTAATTAATCTGCGCCCCCTGGGGAGCCGCCCAACACAGAAATACGATCTGGAGTTG	7080
Qy	7069	ATAACATATAGCTCTCTCCAAATGTGTACGTGCGCAGATATGATCTGGCAAAAGGGTATC	7128
Db	7081	ATAACATATAGCTCTCTCCAAATGTGTACGTGCGCAGATATGATCTGGCAAAAGGGTATC	7140
Qy	7129	TATCTCACCGCGTAGACCCACACCCCTTGGCGGCGGTGCGTGGAGACACTAGACAC	7188
Db	7141	TATCTCACCGCGTAGACCCACACCCCTTGGCGGCGGTGCGTGGAGACACTAGACAC	7200
Qy	7189	ACTCCAGTCAATCTCTGGGCTTAGGCACACATATATGTATGCGCCACCTTGTGGCGAAG	7248
Db	7201	ACTCCAGTCAATCTCTGGGCTTAGGCACACATATATGTATGCGCCACCTTGTGGCGAAG	7260
Qy	7249	ATGATCTGAGTACATCTTCTTCATCCTCTTACCTCAGGAACAATTGAAAAAGCC	7308
Db	7261	ATGATCTGAGTACATCTTCTTCATCCTCTTACCTCAGGAACAATTGAAAAAGCC	7320
Qy	7309	CTAGATTTGTCAAGATCTACGGGGCGCTGTACTCATAGGCACTTACCTACCTCAGATC	7366
Db	7321	CTAGATTTGTCAAGATCTACGGGGCGCTGTACTCATAGGCACTTACCTACCTCAGATC	7380
Qy	7369	ATTCAACACACACAGGCGCTTAGGGCAATTTTCACTCCATAGTTACACTCCAGTGAATC	7428
Db	7381	ATTCAACACACACAGGCGCTTAGGGCAATTTTCACTCCATAGTTACACTCCAGTGAATC	7440
Qy	7429	AATAGGGTGGCTTCACTGAGTCTCAGAAAACTTGGGGTACCGCCCTTGGAGTCTGGAGACAT	7486
Db	7441	AATAGGGTGGCTTCACTGAGTCTCAGAAAACTTGGGGTACCGCCCTTGGAGTCTGGAGACAT	7500
Qy	7489	CGGGCCAGAAAGTGTCCGGGCTAGGCTACTGTGCCAGGGGGGGAGGGGTGCACTTGTGGC	7546
Db	7501	CGGGCCAGAAAGTGTCCGGGCTAGGCTACTGTGCCAGGGGGGGAGGGGTGCACTTGTGGC	7560
Qy	7549	AAGTACCTTTTCACTGAGGCGATAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGG	7608
Db	7561	AAGTACCTTTTCACTGAGGCGATAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGG	7620
Qy	7609	TCCCAATTGGAATTTATCCAGCTGGTGGTGTCTGTGTATCAAGCGGGGAGAGCAATATTCAC	7666
Db	7621	TCCCAATTGGAATTTATCCAGCTGGTGGTGTCTGTGTATCAAGCGGGGAGAGCAATATTCAC	7680
Qy	7669	AGGCTGTCTCGTCCGAGCCCGCTGTGTATGTGTAGTCCCTACTCTTCTGTAGGG	7726
Db	7681	AGGCTGTCTCGTCCGAGCCCGCTGTGTATGTGTAGTCCCTACTCTTCTGTAGGG	7740

[illegible]

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QY 409 ACGAGGTTCTCCGCGCGCTGGTGAGAGGCTATTTCGCAATGACTGGGACAACAGA 468
Db 421 ACGAGGTTCTCCGCGCGCTGGTGAGAGGCTATTTCGCAATGACTGGGACAACAGA 480
QY 469 CAATCGCTGCTGTGATGCCGCGTGTTCGCGCTGTCAAGCGAGGGCGCCGGTTCTTT 528
Db 481 CAATCGCTGCTGTGATGCCGCGTGTTCGCGCTGTCAAGCGAGGGCGCCGGTTCTTT 540
QY 529 TTGTCAAGACCGACCTCTCCGGTGCCCTGMAATGAAGTCCAGAGCGAGGCGGCTAT 588
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DEFINITION	Sequence 2 from Patent EP1043399.				
ACCESSION	AX036253				
VERSION	AX036253.1	GI:1125869			
KEYWORDS					
SOURCE					
ORGANISM	Hepatitis C virus.				
	Hepatitis C virus.				
	viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;				
REFERENCE	1 (bases 1 to 8637)				
AUTHORS	Bartenschlager, R.D.				
TITLE	Hepatitis C virus cell culture system				
JOURNAL	Patent: EP 1043399-A 2 11-OCT-2000;				
	BARTENSCHLAGER RALF DR (DE)				
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	/db_xref="taxon:11103"				
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ORIGIN					
Query Match	91.6% Score 7324.6; DB 6; Length 8637;				
Best Local Similarity	92.5% Pred. No. 0;				
Matches 7985; Conservative	0; Mismatches 4; Indels 648; Gaps				
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Db	1 gccagcccccgcgattggggggcgacactccacatagatcactccctctgagagactactg 60				
QY	tccttcagcagaaagcgtctagcagatggcgttagatagtgctgtcagccacccagagac 120				
Db	61 tccttcagcagaaagcgtctagcagatggcgttagatagtgctgtcagccacccagagac 120				
QY	121 ccccccctccggggagaccatagtgctcgcggaacccggtgagtacacccgaaattgccag 180				
Db	121 ccccccctccggggagaccatagtgctcgcggaacccggtgagtacacccgaaattgccag 180				
QY	131 gacagccgggtcctttcttgatgatacccccgcctcatgctctgagattggcgggcccc 240				
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QY	241 gcgagactgctagccgagtagtgcttgaggcggaagagcccttggtgatactgacctgatagg 300				
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Db	301 gtgcttgccgagtgccccgggagagctctcgtgagacgctgacacatagacacgaatcctaaac 360				
QY	361 ctcaagagaaaacccaagagcgccgcatattggaacaagatggaattggacacagattctc 420				
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D	b	841	TTTCTCATCAGATATATGCAACAAAGATACGGGCTCGAGCACCACTGTTTC	900
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D	b	901	CCAGGCTCAAGGCGCGCATGCGCGACGGCGAGGATCTGCTGTAACCATGCGATGCTT	960
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D	b	1081	TTGGGGGGAATGGGCTACCGCTTCTGCTGCTTAAAGTATGGCGCGCTCCGATTCGC	1140
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D	b	1141	AGCGATTCGCTTCTATGACCTTTCTTACCAATTTCTTGAAGTTTAAACAGACCAACAGC	1200
Q	y	1201	GTTTCCCTTACGGGATCAATTCGCGCTCTCTCTCCCCCCCCCTTAAGTACTGCGC	1260
D	b	1201	GTTTCCCTTACGGGATCAATTCGCGCTCTCTCTCCCCCCCCCTTAAGTACTGCGC	1260
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D	b	1621	TGGCTCTCTCAAGGCTATTCACAAGGGGCTGAAGATGCCAGAAAGTACCCCATTTG	1680
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D	b	1741	AAAGCTAAGSCCCCCCGAAGCACAGGGGAGGTGGTTTTCCTTTGAAAAAACGATATATACC	1800
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D	b	1801	ATGGACCGGAGATGGCAGCATCTGTGCGAGGGCGGTTTTCGTAGTCTGATCTGTTG	1860
Q	y	1804	-----	1803
D	b	1861	ACCTTGACCGCACTATAAGCTGTCTTCGCTAGGCTCATATGTTGGTTACATATTTT	1920
Q	y	1804	-----	1803
D	b	1921	ATCACAGGGCGAGGACACTTGCAAAGTGGATCCCCCCTCAACGTTGGGGGGGC	1980
Q	y	1804	-----	1803
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D	b	2041	AAATCTTGCTCGGCATATCTGCTCCACTCATGTGCTCCAGGCTGATATAACCAAGTG	2100
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D	b	2341	ACCGCGAGTGTGGGACATCTTGAGGCTGCCGCTCCGCGCCAGGGGGAGGGAG	2400
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D	b	2401	ATACATCTGGGAGCCGCGACGACACCTTTGAAGGGCAGGGTGGCGACTCCTTGCGCTATT	2460
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Q	y	1873	CGGACAGGAACAGGTTCAGGGGGAGGTCCAGGTGTCTCCACCAGCAACACATCTTTC	1932
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 Lohmann, V., Koller, F., Koch, J., Herian, U., Theilmann, L. and Bartenschlager, R.
 Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
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QY 601 CGAGGGGGGTTCTTGCACGACTGTCGACGTTGTCACGAGCGGAGGAGGACTGCG 660
Db 601 CGAGGGGGGTTCTTGCACGACTGTCGACGTTGTCACGAGCGGAGGAGGACTGCG 660
QY 661 TCGATATGGGCGAAGTGCAGGCGAGATCTCTGTCATCTCACTTGTCTTCCGAGAG 720
Db 661 TCGATATGGGCGAAGTGCAGGCGAGATCTCTGTCATCTCACTTGTCTTCCGAGAG 720
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QY	721	AAGATTCATCATGCTGTATGCAATGCGGGCGGCTGTCACTACGCTTGATCCGGCTACTGTC	780
Db	721	AAGTATTCATCATGAGCTGTATGCAATGCGGGCGGCTGTCACTACGCTTGATCCGGCTACTGTC	780
QY	781	CATTGCGCCACCAAGAGGAACATCCGATCGAGCGAGCACGTACTCGGATGGAAGCCGATC	840
Db	781	CATTGCGCCACCAAGAGGAACATCCGATCGAGCGAGCACGTACTCGGATGGAAGCCGATC	840
QY	841	TTGTTCGATCAGGATGATCTGTGACAGCAAGACATCAGGGCTTCGGCCACAGCCGAATGTTC	900
Db	841	TTGTTCGATCAGGATGATCTGTGACAGCAAGACATCAGGGCTTCGGCCACAGCCGAATGTTC	900
QY	901	CCAGGCGCAAGGGCCGATAGCCCGAGGAGGATCTGTGTATACCATGAGCATGCT	960
Db	901	CCAGGCGCAAGGGCCGATAGCCCGAGGAGGATCTGTGTATACCATGAGCATGCT	960
QY	961	GCTTGCCGATATCATAGTGTGGAATAATGGCCCTTTTCTGGAATCATGACTGTGGCCGTC	1020
Db	961	GCTTGCCGATATCATAGTGTGGAATAATGGCCCTTTTCTGGAATCATGACTGTGGCCGTC	1020
QY	1021	TGGGTGTGCGGACCGCTATCAAGAGCATAGCTTTGGTCAACCCGTAATATTGCTGAAGAGC	1080
Db	1021	TGGGTGTGCGGACCGCTATCAAGAGCATAGCTTTGGTCAACCCGTAATATTGCTGAAGAGC	1080
QY	1081	TTGGCGGCGAATGGCTGACCGCTTCTCTGTGCTTTAGGGAATCGCGCTCCCGATTCGC	1140
Db	1081	TTGGCGGCGAATGGCTGACCGCTTCTCTGTGCTTTAGGGAATCGCGCTCCCGATTCGC	1140
QY	1141	AGGCGATCGCCTCTATCGCCTTCTTGACAGATCTTCTGATTTAAACAGACCACAAGC	1200
Db	1141	AGGCGATCGCCTCTATCGCCTTCTTGACAGATCTTCTGATTTAAACAGACCACAAGC	1200
QY	1201	GTTTCCCTTAGGGGATCAATTCGCGCCCTCTCCCTCGCCCGCCCGCCCTAAGCTTACGTC	1260
Db	1201	GTTTCCCTTAGGGGATCAATTCGCGCCCTCTCCCTCGCCCGCCCGCCCTAAGCTTACGTC	1260
QY	1261	CGAAGCGCTTGGATTAAGGCGCGTGTGCTTGTCTATATGTTATTTCCACCATATTC	1320
Db	1261	CGAAGCGCTTGGATTAAGGCGCGTGTGCTTGTCTATATGTTATTTCCACCATATTC	1320
QY	1321	CCGATCTTTTGGCAATGTGAAGGGCCGGAACCGGCGCCCTGTCTTTCAGCAGCATTCCT	1380
Db	1321	CCGATCTTTTGGCAATGTGAAGGGCCGGAACCGTGTGCTTTCAGCAGCATTCCT	1380
QY	1381	AGGGGTCTTTCCCTCTCGCCAAAGAAATGCAAGTGTGTGATGTGCTGTGAAGAGCA	1440
Db	1381	AGGGGTCTTTCCCTCTCGCCAAAGAAATGCAAGTGTGTGATGTGCTGTGAAGAGCA	1440
QY	1441	GTTCTCTGGAAGTCTTTTAAGACAAACAAGCTGTAGCAACCTTTGCAAGGAGGAGG	1500
Db	1441	GTTCTCTGGAAGTCTTTTAAGACAAACAAGCTGTAGCAACCTTTGCAAGGAGGAGG	1500
QY	1501	AACCCGCCACTGTGCGACAGGTGCTCTGCGCCAAAGCCACGTAATAGATACACT	1560
Db	1501	AACCCGCCACTGTGCGACAGGTGCTCTGCGCCAAAGCCACGTAATAGATACACT	1560
QY	1561	GCAAAAGGGGACACAACCCAGGTGCAAGTGTAGTGTAGTATGTTAGTCGAAGTAA	1620
Db	1561	GCAAAAGGGGACACAACCCAGGTGCAAGTGTAGTGTAGTATGTTAGTGAAGATCA	1620
QY	1621	TGGCTCTCTCAAGCGTATTCACAAAGGGCTGAAGAGTCCCAAGAGTACCCATTGT	1680
Db	1621	TGGCTCTCTCAAGCGTATTCACAAAGGGCTGAAGAGTCCCAAGAGTACCCATTGT	1680
QY	1681	ATGGATCTGATCTGGGGCCCTCGGTGCAATGCTTACATGATGTTAGTCGAAGTAA	1740
Db	1681	ATGGATCTGATCTGGGGCCCTCGGTGCAATGCTTACATGATGTTAGTCGAAGTAA	1740
QY	1741	AAGCTCTAGGCCCCCGAACCAGGGGACGTGTTTCTCTTTGAAAAACGATATATAC	1800
Db	1741	AAGCTCTAGGCCCCCGAACCAGGGGACGTGTTTCTCTTTGAAAAACGATATATAC	1800

QY	1801	ATG-----	1803
Db	1801	ATGACCGGGAGTGGCAGCATCGTCGGAGGCGGTTTTTGTAAGCTGTGAATCTCTTG	1860
QY	1804	-----	1803
Db	1801	ACCTGTACCGCACTATAAGCTGTCTCTCGTAGGCTCATATGTTGTTACATATTTT	1920
QY	1804	-----	1803
Db	1921	ATCACACAGGCGCGAGCACACTTGCAAAGTGTGATCCCCCCTCAACGTTGCGGGGGC	1980
QY	1804	-----	1803
Db	1991	CGCGATGCCGATCTCTCTCACGTCCGGGATCCACCCAGAGCTATTCTTACCATCAC	2040
QY	1804	-----	1803
Db	2041	AAATCTTGCTCGGCATACTCGGTCCACTATGTGTCTCAAGCTGTATACCAAGTG	2100
QY	1804	-----	1803
Db	2101	CCGACTTCGTGCGCGCACAGGGCTCAATTCGTGCATGCATGCTGTGCGGAAGTTGCT	2160
QY	1804	-----	1803
Db	2161	GGGGTCACTTATGTCCAAATGGCTCATGAAATTGGCCGCACTGACAGTACGAGATT	2220
QY	1804	-----	1803
Db	2221	TATGACATCTACCCCACTCGGAGCTGGGCCACGCGGCTACGAGACCTTGCGGTG	2280
QY	1804	-----	1803
Db	2281	GCAGTTGAGCCCGTCGTCTCTGATATGAGAACCAAGTTATACCTGGGGGGCAGAC	2340
QY	1804	-----	1803
Db	2341	ACCGCGGCTGGGGACATCATTTGGCCTGCCCTCCGCCGCGAGGGGAGGAG	2400
QY	1804	-----	1812
Db	2401	ATACATCTGGGACCGCGCACAGCCTTTGAAGGCGAGGGGTGGCGACTCCTCCGCTATT	2460
QY	1813	ACGGCTACTCTCCCAACAGACGCGAGGCTACTTGGCTGATCATCATAGCCTCAAGGC	1872
Db	2461	ACGGCTACTCTCCCAACAGACGCGAGGCTACTTGGCTGATCATCATAGCCTCAAGGC	2520
QY	1873	CGGGACAGAACAGCTCGAGGGGAGAGTCCAGTGGTCCACGCGAACACAACTTTC	1932
Db	2521	CGGGACAGAACAGCTCGAGGGGAGAGTCCAGTGGTCCACGCGAACACAACTTTC	2580
QY	1933	CTGGGACCTCGATCAATGGCGTGTGTGGACGTCTATCATGTGCGGCTCAAGAGC	1992
Db	2581	CTGGGACCTCGATCAATGGCGTGTGTGGACGTCTATCATGTGCGGCTCAAGAGC	2640
QY	1993	CTTGCCCGGCCAAGGCGCCCATATACCCAATGTATACCAATGTGAGACCGAGACCTGTC	2052
Db	2641	CTTGCCCGGCCAAGGCGCCCATATACCCAATGTATACCAATGTGAGACCGAGACCTGTC	2700
QY	2053	GGCTGCAAGGCGCCCGCGGGGCGCTTCTTGACACCATGTACCTCGCGCAAGCTCGAG	2112
Db	2701	GGCTGCAAGGCGCCCGCGGGGCGCTTCTTGACACCATGTACCTCGCGCAAGCTCGAG	2760
QY	2113	CTTTACTTGTGACGAGGCATGCCATGTATTCGGTGCGCCGGGGGGGCGACAGCAGG	2172
Db	2761	CTTTACTTGTGACGAGGCATGCCATGTATTCGGTGCGCCGGGGGGGCGACAGCAGG	2820
QY	2173	GGGAGCTACTTCCCGCAGGCGCTCTCTACTTGAAGGAGCTTTCGGGCGGCTCCACTG	2232
Db	2821	GGGAGCTACTTCCCGCAGGCGCTCTCTACTTGAAGGAGCTTTCGGGCGGCTCCACTG	2880
QY	2233	CTCTGCCCCCGGGGACGCTGTGGGCTATTTTCGGGCTCCGCTGTGCACCCGAGGGTT	2292

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Db 2881 CTCTGCCCCCTGGGGGACGCTGTGGGCATCTTTGGGCTGCCGTGCACCCAGGGGTT 2940
QY 2293 GCGAAGCGGTGACATTGTGTACCCGTGAGTCTATGGAACCACTATGCGGTCCCGGTC 2352
Db 2941 GCGAAGCGGTGACATTGTGTACCCGTGAGTCTATGGAACCACTATGCGGTCCCGGTC 3000
QY 2353 TTACAGGACAACTGTCCTCCCTCCGGCCGTACCCGACATCTCCAGTGGGCCATCTACAC 2412
Db 3001 TTACAGGACAACTGTCCTCCCTCCGGCCGTACCCGACATCTCCAGTGGGCCATCTACAC 3060
QY 2413 GCCCTACTGTAGCGGCAAGACACTAAGGTGCCGGCTGCTATGCAAGCCCAAGGATAT 2472
Db 3061 GCCCTACTGTAGCGGCAAGACACTAAGGTGCCGGCTGCTATGCAAGCCCAAGGATAT 3120
QY 2473 AAGTGCTTTGCTGAAACCCGTCCGTGCCGCCACCTAGTTTCGGGGCTATATGCT 2532
Db 3121 AAGTGCTTTGCTGAAACCCGTCCGTGCCGCCACCTAGTTTCGGGGCTATATGCT 3180
QY 2533 AAGGACATGATGACACCTAACATGAAACCGGGGTAAGAACATCACACGGGTGCC 2592
Db 3181 AAGGACATGATGACACCTAACATGAAACCGGGGTAAGAACATCACACGGGTGCC 3240
QY 2593 CCCATCAGCTACTCCACTATGGAAGTTTCTGCCAGCGGTGCTCTGCGGGGCC 2652
Db 3241 CCCATCAGCTACTCCACTATGGAAGTTTCTGCCAGCGGTGCTCTGCGGGGCC 3300
QY 2653 TATGACATCATATATGTGATGAGGCGACACTGACTGACCACTATCTCGGGGATC 2712
Db 3301 TATGACATCATATATGTGATGAGGCGACACTGACTGACCACTATCTCGGGGATC 3360
QY 2713 GGCACAGTCTGGACCAAGCGGAGAGCGGCTGGAGCGGACTGCTGTGCCACCGCT 2772
Db 3361 GGCACAGTCTGGACCAAGCGGAGAGCGGCTGGAGCGGACTGCTGTGCCACCGCT 3420
QY 2773 AGCCCTCCGGGATCGGTACCGGTGCCATGCCAACAACATCGAGGAGGTCTGTCCAGC 2832
Db 3421 AGCCCTCCGGGATCGGTACCGGTGCCATGCCAACAACATCGAGGAGGTCTGTCCAGC 3480
QY 2833 ACTGGAAGAATCCCTTTTATGGCAAGCCTCCCATCGAGACCATCAAAGGGGGAGG 2892
Db 3481 ACTGGAAGAATCCCTTTTATGGCAAGCCTCCCATCGAGACCATCAAAGGGGGAGG 3540
QY 2893 CACGTCAATTTCTGCAATTCACAAGAAATGTGATGAGTCGCGCGGAAGCTGTCCGGC 2952
Db 3541 CACGTCAATTTCTGCAATTCACAAGAAATGTGATGAGTCGCGCGGAAGCTGTCCGGC 3600
QY 2953 CTCGGACTCAATGCTGTAGCATATATACCGGGGCTTGATGTATCCGTATACCAACTAGC 3012
Db 3601 CTCGGACTCAATGCTGTAGCATATATACCGGGGCTTGATGTATCCGTATACCAACTAGC 3660
QY 3013 GGAAGAGCTATGTTGCTGAGCAAGAGAGCGCTTAATGACGGGCTTACCGGCGATTTTGAC 3072
Db 3661 GGAAGAGCTATGTTGCTGAGCAAGAGAGCGCTTAATGAGGGGCTTACCGGCGATTTTGAC 3720
QY 3073 TCAGTATGATGATGCAATACATGTGTCAACCCAGACAGTCAGCTCAGCTGGAACCCAGC 3132
Db 3721 TCAGTATGATGATGCAATACATGTGTCAACCCAGACAGTCAGCTCAGCTGGAACCCAGC 3780
QY 3133 TTCAACATTTGAGAGCAAGACGCTGCCACAAGACGCGGTGTACGCTGCCAGCGCGAGGC 3192
Db 3781 TTCAACATTTGAGAGCAAGACGCTGCCACAAGACGCGGTGTACGCTGCCAGCGCGAGGC 3840
QY 3193 AAGAGCTGTAGGGGAGGATGGGCAATTTACAGGTTTGATGACTCCAGGAGAAAGCGGCTCG 3252
Db 3841 AAGAGCTGTAGGGGAGGATGGGCAATTTACAGGTTTGATGACTCCAGGAGAAAGCGGCTCG 3900
QY 3253 GGCATTTGATGATCTCGGTTCTGTGCGAGTGTCTATGACGCGGGGCTGTGTTGATACAG 3312
Db 3901 GGCATTTGATGATCTCGGTTCTGTGCGAGTGTCTATGACGCGGGGCTGTGTTGATACAG 3960
QY 3313 CTCAGCCCGCGAGACCTCAGTTAGTTGGGGCTTACCTAAACACACCGGGGTTGCC 3372
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Db 3961 CTCAGCCCGCGAGACCTCAGTTAGTTGCGGGCTTACTATAACACACAGGTTGCC 4020
QY 3373 GTCTGCGAGACCACTTGAGATCTGAGAGACGCTCTTTACAGGCTCACCCACATAGAC 3432
Db 4021 GTCTGCGAGACCACTTGAGATCTGAGAGACGCTCTTTACAGGCTCACCCACATAGAC 4080
QY 3433 GCCATTTCTGTCCAGACTAAGCAGGCAAGAGACACTTCCCTACCTGGTAGATAC 3492
Db 4081 GCCATTTCTGTCCAGACTAAGCAGGCAAGAGACACTTCCCTACCTGGTAGATAC 4140
QY 3493 CAGGCTACGTTGTGCGCGAGGCTCAGGCTCACCTTCATCTGTTGGAACCAATGTGGAAG 3552
Db 4141 CAGGCTACGTTGTGCGCGAGGCTCAGGCTCACCTTCATCTGTTGGAACCAATGTGGAAG 4200
QY 3553 TGTCTCATAGGGCTTAAGGCTTACGCTGACGCGGCAACGGCCCTGCTGTATAGGCTGGGA 3612
Db 4201 TGTCTCATAGGGCTTAAGGCTTACGCTGACGCGGCAACGGCCCTGCTGTATAGGCTGGGA 4260
QY 3613 GCCGTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATACATCATGATGATGATG 3672
Db 4261 GCCGTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATACATCATGATGATGATG 4320
QY 3673 TCGGCTGACCTGAGAGTCTGACAGACACCTGGGTGCTGGTAGGCGGAGTCTAGACGCT 3732
Db 4321 TCGGCTGACCTGAGAGTCTGACAGACACCTGGGTGCTGGTAGGCGGAGTCTAGACGCT 4380
QY 3733 CTGGCCGCGTATTGCTGTACAAACAGGACGCTGCTATTGTTGGGACAGATCATCTTGTCC 3792
Db 4381 CTGGCCGCGTATTGCTGT 4440
QY 3793 GGAAGCGCGGCATCTATCCCGAAGAGGAACTCTTTACCGGAGTGTGATGAGATGGA 3852
Db 4441 GGAAGCGCGGCATCTATCCCGAAGAGGAACTCTTTACCGGAGTGTGATGAGATGGA 4500
QY 3853 GAGTCCGCTCAACACTCTCTTACATCGAAGAGGAATGACGTGCGGCAAACTTCAAA 3912
Db 4501 GAGTCCGCTCAACACTCTCTTACATCGAAGAGGAATGACGTGCGGCAAACTTCAAA 4560
QY 3913 CAGAAGCAATCGGTTCTCTGCAAAACAGCCACCAAGAGGAGGCTGCTCTCCGCTG 3972
Db 4561 CAGAAGCAATCGGTTCTCTGCAAAACAGCCACCAAGAGGAGGCTGCTCTCCGCTG 4620
QY 3973 GTGGAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATGTAATTTATC 4032
Db 4621 GTGGAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATGTAATTTATC 4680
QY 4033 ACGGGATACATATTTAGAGGCTTGTCACTGCTGCTGGCAACCCCGGATAGATCA 4092
Db 4681 ACGGGATACATATTTAGAGGCTTGTCACTGCTGCTGGCAACCCCGGATAGATCA 4740
QY 4093 CTGATGGAATCACAGCCTCTATACACAGCCCGGCTGACACCAATACCTCTGTTT 4152
Db 4741 CTGATGGAATCACAGCCTCTATACACAGCCCGGCTGACACCAATACCTCTGTTT 4800
QY 4153 AACATCTGGGGGATGGGTGGCCGCCCAACTTCTCTCCAGAGGCTGCTTGTCTTC 4212
Db 4801 AACATCTGGGGGATGGGTGGCCGCCCAACTTCTCTCCAGAGGCTGCTTGTCTTC 4860
QY 4213 GTAGCGCCCGGATCGCTGTGAGCGGCTTGTGGACATAGGCTTGGGAAGTCTGTG 4272
Db 4861 GTAGCGCCCGGATCGCTGTGAGCGGCTTGTGGACATAGGCTTGGGAAGTCTGTG 4920
QY 4273 GATATTTTGGCAGTTATGAGACAGAGGCTGACAGCGGCTGCTGAGCTTTAAGTATG 4332
Db 4921 GATATTTTGGCAGTTATGAGACAGAGGCTGACAGCGGCTGCTGAGCTTTAAGTATG 4980
QY 4333 AAGCGGAGATGCTCTCAACGAGACCTGCTTAACCTACTCCCTGCTATCTCTCCCT 4392
Db 4981 AAGCGGAGATGCTCTCAACGAGACCTGCTTAACCTACTCCCTGCTATCTCTCCCT 5040
QY 4393 GCGGCTTGTGTGCGGCTGTGTGCGACAGATACTGCTGCGACAGTGGGCCCAAGG 4452
Db 5041 GCGGCTTGTGTGCGGCTGTGTGCGACAGATACTGCTGCGACAGTGGGCCCAAGG 5100
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QY	4453	GAGGGGCTGTGCAGTGGATGAAACCGGCTGATAGCTTCGCTTGGCGGGGTAACCAAGTC	4512
Db	5101	GAGGGGCTGTGCAGTGGATGAAACCGGCTGATAGCTTCGCTTGGCGGGGTAACCAAGTC	5160
QY	4513	TCGCCACGACTATGTCCTAGACGCAAGCTGCAGACGTCACATCATCTCTCT	4572
Db	5151	TCGCCACGACTATGTCCTAGACGCAAGCTGCAGACGTCACATCATCTCTCT	5220
QY	4573	AGCTTACCATCACTACGCTGCTGGAAGAGCTTCAACAGTGGATCAACGAGAGCTGTC	4632
Db	5221	AGCTTACCATCACTACGCTGCTGGAAGAGCTTCAACAGTGGATCAACGAGAGCTGTC	5280
QY	4633	ACGCCATGCTCCGGCTGTGGCTAAGATGTTTGGAGTGGATATGACGGTGTACT	4692
Db	5281	ACGCCATGCTCCGGCTGTGGCTAAGATGTTTGGAGTGGATATGACGGTGTACT	5340
QY	4693	GATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCGCGATTGCCGGAGTCCCTTCTTC	4752
Db	5341	GATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCGCGATTGCCGGAGTCCCTTCTTC	5400
QY	4753	TCATGTCAAGTGGGTACAAGGAGCTGCGCGGGCGAGCGGATCATCAACACCTGC	4812
Db	5401	TCATGTCAAGTGGGTACAAGGAGCTGCGCGGGCGAGCGGATCATCAACACCTGC	5460
QY	4813	CCATGTGGAGACAGATCACCGGACATGTGAAAAAGGTTCCATGAGGATGTGGGGCT	4872
Db	5461	CCATGTGGAGACAGATCACCGGACATGTGAAAAAGGTTCCATGAGGATGTGGGGCT	5520
QY	4873	AGGACCTGTGTATACAGTGGGTCATGGAAATTCCTCCATTACGGTATACACGAGGGCCC	4932
Db	5521	AGGACCTGTGTATACAGTGGGTCATGGAAATTCCTCCATTACGGTATACACGAGGGCCC	5580
QY	4933	TGCACGCCCTCCCGCGGCCAAATTTTCTAGGGGCGTGTGGCGGTGGCTGTGAAGAG	4992
Db	5581	TGCACGCCCTCCCGCGGCCAAATTTTCTAGGGGCGTGTGGCGGTGGCTGTGAAGAG	5640
QY	4993	TACCTGAGAGTTACGCGGGTGGGGGATTTCCACTACATGACGGGATACCACTGACAAC	5052
Db	5641	TACCTGAGAGTTACGCGGGTGGGGGATTTCCACTACATGACGGGATACCACTGACAAC	5700
QY	5053	GTAAGTGCCTGTACAGGTTCCGGCCCCCGAATTCCTCACAGAAGTGATGGGGTGGG	5112
Db	5701	GTAAGTGCCTGTACAGGTTCCGGCCCCCGAATTCCTCACAGAAGTGATGGGGTGGG	5760
QY	5113	TTGCACAGTACGCTCCAGGCTGCAAAACCCCTCTACGGGAGAGGTACATTCCTGTGTC	5172
Db	5761	TTGCACAGTACGCTCCAGGCTGCAAAACCCCTCTACGGGAGAGGTACATTCCTGTGTC	5820
QY	5173	GGGCTCATCATATCTGTGTGGTGTACAGCTCCCATGGAGCCCGAACCGGAGTGAACA	5232
Db	5821	GGGCTCATCATATCTGTGTGGTGTACAGCTCCCATGGAGCCCGAACCGGAGTGAACA	5880
QY	5233	GTCCTCACTTCCATGCTCACCGAACCCCTCCACATTTACGGGAGAGCGCTAACGCTAGG	5292
Db	5881	GTCCTCACTTCCATGCTCACCGAACCCCTCCACATTTACGGGAGAGCGCTAACGCTAGG	5940
QY	5293	CTGGCAGAGGGATTCGCCCTCTCTTGGCAGTCATCAGCTAGCACACTTCTGGCCT	5352
Db	5941	CTGGCAGAGGGATTCGCCCTCTCTTGGCAGTCATCAGCTAGCACACTTCTGGCCT	6000
QY	5353	TCCTTGAAGGCACATGCACTACCCGTCATGACTCCCGGAGCGCTGACCTATGAGGCC	5412
Db	6001	TCCTTGAAGGCACATGCACTACCCGTCATGACTCCCGGAGCGCTGACCTATGAGGCC	6060
QY	5413	AACCTCCTGTGGCGCAGAGATGGCGGGAACTACCCCGTGGATCAAGAAATTAAG	5472
Db	6061	AACCTCCTGTGGCGCAGAGATGGCGGGAACTACCCCGTGGATCAAGAAATTAAG	6120
QY	5473	GTAGTAATTTTGACTCTTTTCAGCCGCTCAAGCGGAGAGATGAGAGGAAATATCC	5532
Db	6121	GTAGTAATTTTGACTCTTTTCAGCCGCTCAAGCGGAGAGATGAGAGGAAATATCC	6180

QY	5553	GCGCGGCGGAGANTCCGGCGGAGCTCCAGGAAATTCCTCCGAGGCAATGCCATATPAGGCA	5592
Db	6181	GTCCGCGGGAGATCTCGCGGAGGTCAGAAATTCCTCGAGCATGCCATATGGCA	6240
QY	5593	CGCCCGATTACAAACCCCTCCACTGTTAGATCCTGGAAAGACCCGGACTACGTCCCTCA	5652
Db	6241	CGCCCGATTACAAACCCCTCCACTGTTAGATCCTGGAAAGACCCGGACTACGTCCCTCA	6300
QY	5653	GTGGTACACGGGTGCATTCGCGCGCTCGCAAGGCCCTCCGATPACCACTCCACGGAG	5712
Db	6301	GTGGTACACGGGTGCATTCGCGCGCTCGCAAGGCCCTCCGATPACCACTCCACGGAG	6360
QY	5713	AAGAGGACGGTGTCTGTCGTGAGATCTAACCGTGTCTTGCCCTTGGCGGAGCTGCCCA	5772
Db	6361	AAGAGGACGGTGTCTGTCGTGAGATCTAACCGTGTCTTGCCCTTGGCGGAGCTGCCCA	6420
QY	5773	AAGACCTTGGGAGCTCCGATGCTGCGCGCTGCAGAGGGGACAGGCAAGGCCCTCTCT	5832
Db	6421	AAGACCTTGGGAGCTCCGATGCTGCGCGCTGCAGAGGGGACAGGCAAGGCCCTCTCT	6480
QY	5833	GACCAGCCCTCCGACGACGGCGAGCGGGATCCGAGTTCGAGTGTACTCCTCATGCCC	5892
Db	6481	GACCAGCCCTCCGACGACGGCGAGCGGGATCCGAGTTCGAGTGTACTCCTCATGCCC	6540
QY	5893	CCCCCTTGGGGGGGCGCGGGGGATCCCGATCTCAGAGAGGGTCTTGCTATCCGTATAC	5952
Db	6541	CCCCCTTGGGGGGGCGCGGGGGATCCCGATCTCAGAGAGGGTCTTGCTATCCGTATAC	6600
QY	5953	GAGAGGCTATGAGGACGTCGTCTGCTGCTGATGTCTTACATAGACAGGGGCGCTG	6012
Db	6601	GAGAGGCTATGAGGACGTCGTCTGCTGCTGATGTCTTACATAGACAGGGGCGCTG	6660
QY	6013	ATCACGGCATGCGCTGCGGAGGAAACCAAGCTGCCATTAATGCACTGACACCTCTTG	6072
Db	6661	ATCACGGCATGCGCTGCGGAGGAAACCAAGCTGCCATTAATGCACTGACACCTCTTG	6720
QY	6073	CTCCGTACCAACAATTGTCTATGCTACAACTCTCGACGCGCAAGCCTGGGCGAG	6132
Db	6721	CTCCGTACCAACAATTGTCTATGCTACAACTCTCGACGCGCGCAAGCCTGGGCGAG	6780
QY	6133	AAGGTCACCTTGTGACACTAGCAGAGTCTCTGAGACCACTACCGGAGCTGCTCAAGAG	6192
Db	6781	AAGGTCACCTTGTGACACTAGCAGAGTCTCTGAGACCACTACCGGAGCTGCTCAAGAG	6840
QY	6193	ATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGGAGAGACCTGTAG	6252
Db	6841	ATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGGAGAGACCTGTAG	6900
QY	6253	CTGAGCGCCCCCACTTGGGCGCAATCTAATTTGGGTATGGGGCAAGAGAGCTCCGAGAC	6312
Db	6901	CTGAGCGCCCCCACTTGGGCGCAATCTAATTTGGGTATGGGGCAAGAGAGCTCCGAGAC	6960
QY	6313	CTATCCAGACAGGCGGTTAAACAATCCGCTCGTGTGGAAGAGACTTGTGGAAGACACT	6372
Db	6961	CTATCCAGACAGGCGGTTAAACAATCCGCTCGTGTGGAAGAGACTTGTGGAAGACACT	7020
QY	6373	GAGACACCAATTGTACACCACTATCATGGCAAAATAAGAGTTTCTGCGTCCACAACAGAG	6432
Db	7021	GAGACACCAATTGTACACCACTATCATGGCAAAATAAGAGTTTCTGCGTCCACAACAGAG	7080
QY	6433	AAGGGGGGCGCAAGCCAGCTCGGCTTATCGTATTCCTCCAGATTTGGGGTTCGTGTGCG	6492
Db	7081	AAGGGGGGCGCAAGCCAGCTCGGCTTATCGTATTCCTCCAGATTTGGGGTTCGTGTGCG	7140
QY	6493	GAGAAATGAGCCCTTACGATGTGTGTCACCCCTCCACAGCGGTGATGGGCTCTTCA	6552
Db	7141	GAGAAATGAGCCCTTACGATGTGTGTCACCCCTCCACAGCGGTGATGGGCTCTTCA	7200
QY	6553	TACGGATTCAAATCTCTCTCGACAGCGGGTGAATTCCTGTGTGAATTCCTGGAAACGG	6612
Db	7201	TACGGATTCAAATCTCTCTCGACAGCGGGTGAATTCCTGTGTGAATTCCTGGAAACGG	7260
QY	6613	AAGAAATCCCTATGGGCTTCGATATGAACCCCGGTGTTTGTAGACTCAACGGTCTCACTAG	6672

Db 7261 AAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTGACCAAGGTCACTAG 7320
 Qy 6673 AATGACATCCGCTGTTGAGAGATCTACCAATGTTGTGACTTGSCCCCGAGAGCCAGA 6732
 Db 7321 AATGACATCCGCTGTTGAGAGATCTACCAATGTTGTGACTTGSCCCCGAGAGCCAGA 7380
 Qy 6733 CAGGCCATTAAGTGGCTCAGAGAGGCGCTTACATGSGGGGCCCCGTGACTATTTCTAA 6792
 Db 7381 CAGGCCATTAAGTGGCTCAGAGAGGCGCTTACATGSGGGGCCCCGTGACTATTTCTAA 7440
 Qy 6793 GGGCAGAACTGCGCTATCCCGGCTGCGCGAGCGGCTGCTACTGACGACAGCTGCGGT 6852
 Db 7441 GGGCAGAACTGCGCTATCCCGGCTGCGCGAGCGGCTGCTACTGACGACAGCTGCGGT 7500
 Qy 6853 AATACCCCTCANAATGTTACTTGAAGGCGCGCTGCGAGCTGCGAGCTGCGAGCTGCGAG 6912
 Db 7501 AATACCCCTCANAATGTTACTTGAAGGCGCGCTGCGAGCTGCGAGCTGCGAGCTGCGAG 7560
 Qy 6913 TGCACGATGCTGCTATGCGGAGAGACCTTGTGTTATCTGTGAAGCGCGGAGACCAA 6972
 Db 7561 TGCACGATGCTGCTATGCGGAGAGACCTTGTGTTATCTGTGAAGCGCGGAGACCAA 7620
 Qy 6973 GAGGACGAGCGGAGCTTACGCGGCTTACGAGAGCTATGACTGATACCTGCCCCCT 7032
 Db 7621 GAGGACGAGCGGAGCTTACGCGGCTTACGAGAGCTATGACTGATACCTGCCCCCT 7680
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 Hepatitis C virus
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 Hepacivirus.
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 AUTHORS Bartenschlager R.D.
 TITLE Hepatitis C virus cell culture system
 JOURNAL Patent: EP 1043399-A 5 11-OCT-2000;
 BARTENSCHLAGER RALF DR (DE)
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 ORIGIN

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VERSION AJ242653.1 GI:5441837
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ORGANISM Hepatitis C virus replicon I389/NS2-3'UTR.
REFERENCE 1 (bases 1 to 8649)
AUTHORS Lohmann,V., Korte,F., Koch,J., Herian,U., Theilmann,L. and Bartenschlager,R.
TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
JOURNAL Science 285 (5424), 110-113 (1999)
MEDLINE 59322193
PUBMED 10390360
REFERENCE 2 (bases 1 to 8649)
AUTHORS Bartenschlager,R.
TITLE Direct Submision
JOURNAL Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY
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 SOURCE Hepatitis C virus.
 ORGANISM Hepatitis C virus.
 Viruses; ssRNA positive-strand viruses, no DNA stage: Flaviviridae; Hepacivirus.
 REFERENCE 1
 AUTHORS Kukulj, G. and Pause, A.
 TITLE Self-replicating rna molecule from hepatitis C virus
 JOURNAL Patent: WO 02052015-A-1 04-JUL-2002.
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D	8151	GTCGCGCTAGGCTACTGTCCAGGGGGAGGCGTGCACCTGTGGCAATGACTCTTC	8210
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OY	7621	TTATCCAGCTGTGTGGTGTCTGTATACAGCGGGGAGACATATATCACAGCCTGTCTGT	7680
D	8271	TTATCCAGCTGTGTGGTGTCTGTATACAGCGGGGAGACATATATCACAGCCTGTCTGT	8330
OY	7681	GCCGACCCCCGCTGCTATATGAGTGCCTACTCCTACTTCTCTAGGGGTAGGAAATAT	7740
D	8331	GCCGACCCCCGCTGCTATATGAGTGCCTACTCCTACTTCTCTAGGGGTAGGAAATAT	8390
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D	8451	TTTCCCTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTTT	8510
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LOCUS	Sequence 24 from Patent WO02052015.		
DEFINITION	AX472314		
ACCESSION	AX472314		
VERSION	AX472314.1	GI:22207333	
KEYWORDS			
SOURCE	Hepatitis C virus. Hepatitis C virus. Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepadnavirus.		
ORGANISM			
REFERENCE	1		
AUTHORS	Kukolj,G. and Pause,A.		
TITLE	Self-replicating rna molecule from hepatitis C virus		
JOURNAL	Patent: WO 02052015-A 24 04-JUL-2002;		
	BOEHRINGER INGENLHEIM (CANADA) LTD. (CA)		
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[illegible]

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 DB 602 GACGGGGGCTTCCTTGGCAGCTGTGCTCGACGTTGTCTACTGAAGCGGGAAGGACTGGCT 661
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 DB 662 GCTATTGGGGGAAGTGGCGGGGAGGATTCCTGTATCATCATCACTTGCCTCGCGAGAA 721
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 DB 722 AGTATTCATCATGAGCTGATGCAATGGCGGCGCTGATACGCTTGATCGCGTACCTGCC 781
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 DB 842 TGTGATCAGAGTATGATCGACGAGAGCATCAGGGGCTGCGCCAGCGAACTGTTCG 901
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QY 6422 TCAACCAAGAGAGGGGGCGGCAAGCCAGCTGCTTATGCTATTTCCAGATTTGGGG 6481

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Oy	6482	TTGCTGTGTCGAGAAAATGCCCCCTTTACGATGTGCTCCACCCCTCCCTCAGGCCGTGA	6541
Db	7131	TTGCTGTGTGCGGAAAAATGGCCCTTTAGAGTGTGTCACACCCCTCCCTCAGGCCGTGA	7190
Oy	6542	TGGGCTTTTCATACGGAATTCCAATACTCTCTCCGAGCAGCAGCGGTGAGTCTCTGTGTGATG	6601
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Db	7251	CTTGAAGACGGAAGAAATGCCCTATGCGCTTGCAATATGACACCCGCTGTTTACTGCA	7310
Oy	6662	CGGTCATAGATGATGACATCCGCTGTGAGAGATCAATATACCAATGTGTGACTTGGCCC	6721
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Oy	6722	CCGAAAGCCAGACAGGCCATTAAGTGCCTACAGAGCGGCTTTACTATGGGGGGCCCCCTGA	6781
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Oy	6782	CTAATTTAAAGGACAGAAATGCGGGCTATCGCCGGTGCCGCGCAGCGGTGTACTGACGA	6841
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Oy	6842	CCAGCTCGGTAATACCTCTACATGTTACTTGAAGCGCGTCTGGCCCTGTGAGCTAGCGGA	6901
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Oy	6902	AGCTCCAGGACTGCAACAGTCTGTATGCGGAGACACCTTCTCTTATCTGTGAACCG	6961
Db	7551	AGCTCCAGGACTGCAACAGTCTGTATGCGGAGACACCTTCTCTTATCTGTGAACCG	7610
Oy	6962	CGGGAGCCCAAGAGAGACAGAGCCCAAGCCCTTACAGGAGGCTATGAGTATGAT	7021
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Db	7671	CTGGCCCCCCTGGGGAGACCCGCCCAACACAGAAATACGACTTGGAGTTGATTAACATCATGCT	7730
Oy	7082	CCTGCAATGTGTCAAGTGGGGCAGATGSCATCTGGCAAAAGGGTATCTTCACCCGTG	7141
Db	7731	CCTGCAATGTGTCAAGTGGGGCAGATGSCATCTGGCAAAAGGGTATCTTCACCCGTG	7790
Oy	7142	ACCCACACACCCCTTTCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCATGCAAT	7201
Db	7791	ACCCACACACCCCTTTCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCATGCAAT	7850
Oy	7202	CCTGGCTAGGGAACATATATATGATGCGGCCACTTGTGGGGAAGAGATCTCGAAGA	7261
Db	7851	CCTGGCTAGGGAACATATATGATGCGGCCACTTGTGGGGAAGAGATCTCGAAGA	7910
Oy	7262	CTCATTTCTTCCATCCTTCTAGCTCAGAACACTTGAAAAAGCCCTAGATTGTGAGA	7321
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Oy	7322	TCTTACGGGGGCTGTACTTCATTCATGAGCACTTGACACTCGACTCGATTCACAGACATCC	7381
Db	7971	TCTTACGGGGGCTGTACTTCATTCATGAGCACTTGACACTCGACTCGATTCACAGACATCC	8030
Oy	7382	ATGGCCTTAGGCAATTTTCACTCCATAGTACTCTCCAGGTGATCAATAGGTGTGCTT	7441
Db	8031	ATGGCCTTAGGCAATTTTCACTCCATAGTACTCTCCAGGTGATCAATAGGTGTGCTT	8090
Oy	7442	CATGGCTCAGGAAATTGGGGTACCGGCTTGAGAGTCTGGAGACATCGGGCCAGAAAG	7501
Db	8091	CATGGCTCAGGAAATTGGGGTACCGGCTTGAGAGTCTGGAGACATCGGGCCAGAAAG	8150
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[illegible]

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Qy	1804	-----	1803
Db	1850	CTGATCTCTTGACCTGTACCGGACATATAAGCTTTCTCGGTAGGCTCATATGTTG	1909
Qy	1804	-----	1803
Db	1910	TTACATATTTTATCACAGGGGCGGAGGACACTTGAAGTGTGATGCCCCCTCAAC	1969
Qy	1804	-----	1803
Db	1970	GTTCGGGGGGCGGATGCCGATCTCTCTCACGTGCGGATCCACAGAGCTATAC	2029
Qy	1804	-----	1803
Db	2030	TTTACATACACAAAATCTTGTCGCGACATACGTGCTCCACTCATGTGGTCTCAAGTGGT	2089
Qy	1804	-----	1803
Db	2090	ATAACAAAGTGCCGCTACTTGTGCGGACAGGGGCTCAFTTCGTGATGATGCTGTG	2149
Qy	1804	-----	1803
Db	2150	CGGAAGTTGCTGGGGTCAATTATGTCAAATGGCTCTCATGAAGTTGGCGCACTGACA	2209
Qy	1804	-----	1803
Db	2210	GGTACGTACGTTTATGACATCTACCCCACTGCGGGACTGGGCCACGCGGGCTTACGA	2269
Qy	1804	-----	1803
Db	2270	GACCTGCGGTGGGAGTGTAGCCCGTCTCTTCTGTGATGAGAGACCAAGTTATGACC	2329
Qy	1804	-----	1803
Db	2330	TGGGGGCGAGACACCGCGGCTGTGGGACATCACTTGGGCTGCCCTCCGCGCCGC	2389
Qy	1804	-----	1803
Db	2390	AGGGGAGGGGATACATCTGGGACCGGACGAGACAGCTTGAAGGCGAGGGGTGGCGATC	2449
Qy	1804	---GCGCTATTAGGCTTACTTCCCAACAGAGCGCTACCTGGCTGGATCATACT	1860
Db	2450	CTCGGCTATTAGGCTACTCTCCACACAGCGAGGCTTACTTGGCTGATCATCAC	2509
Qy	1861	AGCCTCACAGGCCGCGACAGAAACCAAGTGTGAGGGGAGGTCAGGTGCTCCACGCA	1920
Db	2510	AGCCTCACAGGCCGCGACAGAAACCAAGTGTGAGGGGAGGTCAGGTGCTCCACGCA	2569
Qy	1921	ACACAACTTTCTGGGGGACTCGCTCAATAGGGGTGTGTGAGCTGTCATCATAGTATC	1980
Db	2570	ACACAACTTTCTGGGGGACTCGCTCAATAGGGGTGTGTGAGCTGTCATCATAGTATC	2629
Qy	1981	GGCTTAAAGACCTTGGCGGCCAAAGAGGCCCATCACCAATGTACACCAATGTGAC	2040
Db	2630	GGCTTAAAGACCTTGGCGGCCAAAGAGGCCCATCACCAATGTACACCAATGTGAC	2689
Qy	2041	CAGGACCTGTCGGGTGGCAAGGGGCGGGGGCGGCTTCTGTGACACATGACCTGC	2100
Db	2690	CAGGACCTGTCGGGTGGCAAGGGGCGGGGGCGGCTTCTGTGACACATGACCTGC	2749
Qy	2101	GGGACCTGGACCTTACTTGTGTACAGAGCATGCGATGTCAATTCGGTGGCGCGCG	2160

Dh	2750	GGCGAGCTCGGAGACCTTTACTTTGGTACAGAAAGCATGCGATGTGATTCGGTGGCGCGGCGG	2800
Qy	2161	GGGACAGCAGAGGGGGAGGACCTACTCTCTCCCCAGAGGCCGATCTCTACTTAAAGGCTCTTG	2220
Dh	2810	GGGACAGCAGAGGGGGAGGACCTACTCTCTCCCCAGAGGCCGATCTCTACTTAAAGGCTCTTG	2869
Qy	2221	GGCGGTCACACTGCTCTGCCCTCTCGGGGACAGCTGTGGGCACTTTTCGGGCTGCCGTGTG	2280
Dh	2870	GGCGGTCACACTGCTCTGCCCTCTCGGGGACAGCTGTGGGCACTTTTCGGGCGCGGTGTG	2929
Qy	2281	ACCCGAGGGGTTGGAAGGGGGGTGAAGGACTTTGTACCCGTCGAGTCAITGGAAACCACTATG	2340
Dh	2930	ACCCGAGGGGTTGGAAGGGGGGTGAAGGACTTTGTACCCGTCGAGTCAITGGAAACCACTATG	2999
Qy	2341	CGGTCCCGGCTCTTCACGAGCAACTGTCGCCCTCCGGCCGTACGGCAGACATTTCCAGTG	2400
Dh	2990	CGGTCCCGGCTCTTCACGAGCAACTGTCGCCCTCCGGCCGTACGGCAGACATTTCCAGTG	3049
Qy	2401	GGCCATCTACACGCCCCCTACTGCTAGCGGACAGACACTAAAGSTGCCGCTGCTATGCA	2460
Dh	3050	GGCCATCTACACGCCCCCTACTGCTAGCGGACAGACACTAAAGSTGCCGCTGCTATGCA	3109
Qy	2461	GCCCCAGGGTAAAGTGCTTTGCTCTGAACCCGTCGCGCCACCCCTAGTTTCGGG	2520
Dh	3110	GCCCCAGGGTAAAGTGCTTTGCTCTGAACCCGTCGCGCCACCCCTAGTTTCGGG	3169
Qy	2521	GGCATATATGCTAAGGACACTGTGTATCGAACCCCAATAGACAGCCGGGTAAAGACATC	2580
Dh	3170	GGCATATATGCTAAGGACACTGTGTATCGAACCCCAATAGACAGCCGGGTAAAGACATC	3229
Qy	2581	ACCACGGGTGCCCCATACGCTACTCCACCTATGGCASTTTTCTTGGCAGGGGTGTTC	2640
Dh	3230	ACCACGGGTGCCCCATACGCTACTCCACCTATGGCASTTTTCTTGGCAGGGGTGTTC	3289
Qy	2641	TCTGGGGGCGCTATGATCATATATATGATGATGAGATGCGACCTCACTACGACGCACT	2700
Dh	3290	TCTGGGGGCGCTATGATCATATATATGATGATGAGATGCGACCTCACTACGACGCACT	3349
Qy	2701	ATCTGGGATGCGCACATGCTCTGAGACCAAGCGGAGAGGGCTGGAGCGCGACTGCTGTG	2760
Dh	3350	ATCTGGGATGCGCGCACATGCTCTGAGACCAAGCGGAGAGGGCTGGAGCGCGACTGCTGTG	3409
Qy	2761	CTCGCACCGCTTAGCGCTCTCGGGATGAGTCAACGTGCCACATCCAAACATCGAGGAGGTG	2820
Dh	3410	CTCGCACCGCTTAGCGCTCTCGGGATGAGTCAACGTGCCACATCCAAACATCGAGGAGGTG	3469
Qy	2821	GCTCTGTCAACACTGAGAAATCCCTTTTATGGCAAGCCATCCCATGAGACCACTG	2880
Dh	3470	GCTCTGTCAACACTGAGAAATCCCTTTTATGGCAAGCCATCCCATGAGACCACTG	3529
Qy	2881	AAGGGGAGGAGCAACCTATTTCTGCAATCCCAAGAAATATGTATGAGTCCGCGG	2940
Dh	3530	AAGGGGAGGAGCAACCTATTTCTGCAATCCCAAGAAATATGTATGAGTCCGCGG	3589
Qy	2941	AAGGTCTCGGACCTCGGACTCAATGCTGTAGCATATTACCGGGGCGTTGATATTCGTC	3000
Dh	3590	AAGGTCTCGGACCTCGGACTCAATGCTGTAGCATATTACCGGGGCGTTGATATTCGTC	3649
Qy	3001	ATACCACTACCGGAGAGCTATTTGCTGTAGCAAGAGAGCTCTAATGACGGGCTTTAC	3060
Dh	3650	ATACCACTACCGGAGAGCTATTTGCTGTAGCAAGAGAGCTCTAATGACGGGCTTTAC	3709
Qy	3061	GGCGATTTTGACTCAGTATGATGATGAAATACATGTGTACCCGAGCACTGACTTCAAGC	3120
Dh	3710	GGCGATTTTGACTCAGTATGATGATGAAATACATGTGTACCCGAGCACTGACTTCAAGC	3769
Qy	3121	CTGGAACCGGACTTCACCATTTGAGACGAGACCGGTGCACAAAGACCGGCTGACGCTG	3180
Dh	3770	CTGGAACCGGACTTCACCATTTGAGACGAGACCGGTGCACAAAGACCGGCTGACGCTG	3829
Qy	3181	CAGCGGACAGGACAGGACTGATGATGGGAGAGTGGGCACTTACAGGTTTGTGACTCCAGA	3240
Dh	3830	CAGCGGACAGGACAGGACTGATGATGGGAGAGTGGGCACTTACAGGTTTGTGACTCCAGA	3889

QY 3241 GAAGGCCCTCGGCGATGTTGATTCCTCGGTTCTGTGCGAGTGTATGAGCGGGGCTGT 3300
| | | | |
Db 3890 GAACGGCCCTCGGGGATGTTGATTCCTCGGTTCTGTGCGAGTGTATGAGCGGGGCTGT 3949
| | | | |
QY 3301 GCTTGATGAGCTCAGCGCCCGGAGACCTCAGTAGGTGCGGGCTTACTTAACACA 3360
| | | | |
Db 3950 GCTTGATGAGCTCAGCGCCCGGAGACCTCAGTAGGTGCGGGCTTACTTAACACA 4009
| | | | |
QY 3361 CCAGGTTCCCGTCTGCCAGGACATCGAGTTCTGGGAGAGGCTTTACAGGCTC 3420
| | | | |
Db 4010 CCAGGTTCCCGTCTGCCAGGACATCGAGTTCTGGGAGAGGCTTTACAGGCTC 4069
| | | | |
QY 3421 ACCCAATFAGAGCCCATTTCTGTCCGAGTAAAGGAGGAGAGCACTTCCCTAC 3480
| | | | |
Db 4070 ACCCAATFAGAGCCCATTTCTGTCCGAGTAAAGGAGGAGAGCACTTCCCTAC 4129
| | | | |
QY 3481 CTGGTAGCATACCAAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACTCCATCGTGGAC 3540
| | | | |
Db 4130 CTGGTAGCATACCAAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACTCCATCGTGGAC 4189
| | | | |
QY 3541 CAATATGGAGAGTGTCTCATAGGGCTAAAGCCTACGCTGACAGGAGCAAGCGCCCTGCTG 3600
| | | | |
Db 4190 CAATATGGAGAGTGTCTCATAGGGCTAAAGCCTACGCTGACAGGAGCAAGCGCCCTGCTG 4249
| | | | |
QY 3601 TATAGGCTGGAGCCGTTCAAAAAGAGTTACTACCAACACCCCAATACCAATACATC 3660
| | | | |
Db 4250 TATAGGCTGGAGCCGTTCAAAAAGAGTTACTACCAACACCCCAATACCAATACATC 4309
| | | | |
QY 3661 ATGGCATGCTGTGCGGCTACCTGAGGAGTGTGTCAGAGACCTGGGTGTGTTAGCGGA 3720
| | | | |
Db 4310 ATGGCATGCTGTGCGGCTACCTGAGGAGTGTGTCAGAGACCTGGGTGTGTTAGCGGA 4369
| | | | |
QY 3721 GTCTACGACCTCTGGCCGCGCTATTGCTGTACAAACAGGAGCGGTGTGTGTGGGAGG 3780
| | | | |
Db 4370 GTCTACGACCTCTGGGTGTGCTGTGCTGTACAAACAGGAGCGGTGTGTGTGGGAGG 4429
| | | | |
QY 3781 ATCATCTGTGCGGAGGCGCGGACATCTCCGAGAGGAGTCTTTACGGGAGGATC 3840
| | | | |
Db 4430 ATCATCTGTGCGGAGGCGCGGACATCTCCGAGAGGAGTCTTTACGGGAGGATC 4489
| | | | |
QY 3841 GATGAGATGAGAGAGTGCCTGCTACACCTCCCTTACATGAACAGAGGAGTGCAGCTGCGC 3900
| | | | |
Db 4490 GATGAGATGAGAGAGTGCCTGCTACACCTCCCTTACATGAACAGAGGAGTGCAGCTGCGC 4549
| | | | |
QY 3901 GAAATATTCAACAGAAAGGCAATCGGGTGTGCTGCAAAAGCCACCAAGCAAGCGAGGCT 3960
| | | | |
Db 4550 GAAATATTCAACAGAAAGGCAATCGGGTGTGCTGCAAAAGCCACCAAGCAAGCGAGGCT 4609
| | | | |
QY 3961 GCTCTCCGCGTGGTAATCAAGTGGAGGACCTCGAAGCCTTTCGGGCGAAGATATG 4020
| | | | |
Db 4610 GCTCTCCGCGTGGTAATCAAGTGGAGGACCTCGAAGCCTTTCGGGCGAAGATATG 4669
| | | | |
QY 4021 TGGATTTTCATCAGCGGAGTACAAATATTGACAGGCTTGTCCACTGCTGCGCAACCCG 4080
| | | | |
Db 4670 TGGATTTTCATCAGCGGAGTACAAATATTGACAGGCTTGTCCACTGCTGCGCAACCCG 4729
| | | | |
QY 4081 GCGATGAGATCAGTATGATGATTCACAGCTCTATCACAGCCCGCTACCAACCAAT 4140
| | | | |
Db 4730 GCGATGAGATCAGTATGATGATTCACAGCTCTATCACAGCCCGCTACCAACCAAT 4789
| | | | |
QY 4141 ACCCTCTGTTTAAACATCTGAGGAGGAGTGGGTGGCGCCCACTTGTCTCTCCAGGCT 4200
| | | | |
Db 4790 ACCCTCTGTTTAAACATCTGAGGAGGAGTGGGTGGCGCCCACTTGTCTCTCCAGGCT 4849
| | | | |
QY 4201 GCTTCTGCTTCTGAGGAGCGGAGCATGCTGAGGAGGCTTGTGGCAGCATAGGCTTGGG 4260
| | | | |
Db 4850 GCTTCTGCTTCTGAGGAGCGGAGCATGCTGAGGAGGCTTGTGGCAGCATAGGCTTGGG 4909
| | | | |
QY 4261 AAGGTCTTGTGATATTTTGGAGGTTATGAGAGCAAGGAGTGCAGGCGCTGTGGCC 4320
| | | | |
Db 4910 AAGGTCTTGTGATATTTTGGAGGTTATGAGAGCAAGGAGTGCAGGCGCTGTGGCC 4969
| | | | |

QY 4321 TTTAAGTATAGAGCGGAGAGTGCCTTCACCCAGGAGCCTGAGTAACCTACTCCCTGCT 4380
| | | | |
Db 4970 TTTAAGTATAGAGCGGAGAGTGCCTTCACCCAGGAGCCTGAGTAACCTACTCCCTGCT 5029
| | | | |
QY 4381 ATCTCTCCCTGCGGCGCTAGTGTGCGGGTCTGTGCGAGGATACCTGCGGAC 4440
| | | | |
Db 5030 ATCTCTCCCTGCGGCGCTAGTGTGCGGGTCTGTGCGAGGATACCTGCGGAC 5089
| | | | |
QY 4441 GTGGGCGGAGGAGGAGGCTGTGAGTGAATGAACCGGCTGATAGCGTTTCCGCGG 4500
| | | | |
Db 5090 GTGGGCGGAGGAGGAGGCTGTGAGTGAATGAACCGGCTGATAGCGTTTCCGCGG 5149
| | | | |
QY 4501 GGTAAACAGCTGTCCCCACGCACTATGTGCTTGAAGACGAGCTGCACAGCTGTACT 4560
| | | | |
Db 5150 GGTAAACAGCTGTCCCCACGCACTATGTGCTTGAAGACGAGCTGCACAGCTGTACT 5209
| | | | |
QY 4561 CAGATCCTGTAGTCTTACCATCATCAGAGTGTGAAGAGGCTTCCACAGTGAATCAAC 4620
| | | | |
Db 5210 CAGATCCTGTAGTCTTACCATCATCAGAGTGTGAAGAGGCTTCCACAGTGAATCAAC 5269
| | | | |
QY 4621 GAGAGCTGTCCACGCGCATGTCCGGCTGTGGCTAAGAGATGTTGGGATTTGATATGC 4680
| | | | |
Db 5270 GAGAGCTGTCCACGCGCATGTCCGGCTGTGGCTAAGAGATGTTGGGATTTGATATGC 5329
| | | | |
QY 4681 ACGGTGTGACATGATTTCAAGACCTGGCTCCAGTCCCAAGCTCCGCGGAGTGGCGGGA 4740
| | | | |
Db 5330 ACGGTGTGACATGATTTCAAGACCTGGCTCCAGTCCCAAGCTCCGCGGAGTGGCGGGA 5389
| | | | |
QY 4741 GTCCCTCTTCTCATGTCAACGTGGGTACAAGGAGTGTGGCGGAGCGGACATATG 4800
| | | | |
Db 5390 GTCCCTCTTCTCATGTCAACGTGGGTACAAGGAGTGTGGCGGAGCGGACATATG 5449
| | | | |
QY 4801 CAACACACCTGCCAGTGTGAGCAGACAGATCACCGGACATGTGAAGAGGTTCCATGAGG 4860
| | | | |
Db 5450 CAACACACCTGCCAGTGTGAGCAGACAGATCACCGGACATGTGAAGAGGTTCCATGAGG 5509
| | | | |
QY 4861 ATGCTGGGAGCTAGGACCTGTAGTAAACAGTGGATGGAACATTCGCCATTAACCGGTAC 4920
| | | | |
Db 5510 ATGCTGGGAGCTAGGACCTGTAGTAAACAGTGGATGGAACATTCGCCATTAACCGGTAC 5569
| | | | |
QY 4921 ACCACGAGGCGCCCTGCAAGCCCTCCCGGCGCCCAATATTCTTAAGGAGGCTGTGGCGGTG 4980
| | | | |
Db 5570 ACCACGAGGCGCCCTGCAAGCCCTCCCGGCGCCCAATATTCTTAAGGAGGCTGTGGCGGTG 5629
| | | | |
QY 4981 GCTGCTAGAGAGTACGTGAGGTTTACCGCGGTGGGAGTTTCCACTAGGTGACGGGATG 5040
| | | | |
Db 5630 GCTGCTAGAGAGTACGTGAGGTTTACCGCGGTGGGAGTTTCCACTAGGTGACGGGATG 5689
| | | | |
QY 5041 ACCACTGACAGCTAAAGTCCCGTGTCAAGTTCGGGCGCCCGGAATTTCTTCACAAAGT 5100
| | | | |
Db 5690 ACCACTGACAGCTAAAGTCCCGTGTCAAGTTCGGGCGCCCGGAATTTCTTCACAAAGT 5749
| | | | |
QY 5101 GATGGGCTGGGTTTGCACAGTACGCTCCAGGCTGCAAAACCCCTCTACGGGAGGAGTGC 5160
| | | | |
Db 5750 GATGGGCTGGGTTTGCACAGTACGCTCCAGGCTGCAAAACCCCTCTACGGGAGGAGTGC 5809
| | | | |
QY 5161 ACATTTCTGTGCGGCTCAATCAATACCTGTGTTGGGTGCACAGCTCCCATGCGAGCCGAA 5220
| | | | |
Db 5810 ACATTTCTGTGCGGCTCAATCAATACCTGTGTTGGGTGCACAGCTCCCATGCGAGCCGAA 5869
| | | | |
QY 5221 CCGAGGTAGAGTGTGATTCATCATAGTGTACCGGACCCCTCCACATTAACGCGGAGAGG 5280
| | | | |
Db 5870 CCGAGGTAGAGTGTGATTCATCATAGTGTACCGGACCCCTCCACATTAACGCGGAGAGG 5929
| | | | |
QY 5281 GCTAAGGCTAGAGTGTGCGGAGGAGTGTCCCTCTTGGCCAGCTCATACCTAGCCAG 5340
| | | | |
Db 5930 GCTAAGGCTAGAGTGTGCGGAGGAGTGTCCCTCTTGGCCAGCTCATACCTAGCCAG 5989
| | | | |
QY 5341 CTGTCTGGGCTTCTTGAAGGCAACATGCACTACCGCTATGACTCCCGGAGCGCTGAC 5400
| | | | |
Db 5990 CTGTCTGGGCTTCTTGAAGGCAACATGCACTACCGCTATGACTCCCGGAGCGCTGAC 6049
| | | | |
QY 5401 CTGATCGAGGCAACCTCTGTGTGGCGGAGAGTGGCGGAGACATCAACCCGCGTGGAG 5460
| | | | |

Db	6050	CTCATCGAGGCCAACCTCCTGTGGCGGCGAGAGATGSGCGGAACTACACCCGCGTGGAG		6109
Qy	5461	TCACAAATATAGGTAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGAGAGATGAG		5520
Db	6110	TCAGAGATATAGGAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGAGAGATGAG		6169
Qy	5521	AGGGAATATCCGCTTCCGGCGAGATCTCTGGCGAGGTCTCAGAAATTCCTCCGAGGATG		5580
Db	6170	AGGGAATATCCGCTTCCGGCGAGATCTCTGGCGAGGTCTCAGAAATTCCTCCGAGGATG		6229
Qy-	5581	CCCATATAGGCGAGCCCGGATTTCAAACCTCTCACAGTATAGAGTCTCTGGAAGGAAACCGGAC		5640
Db	6230	CCCATATAGGCGAGCCCGGATTTCAAACCTCTCACAGTATAGAGTCTCTGGAAGGAAACCGGAC		6289
Qy	5641	TACGTCCTCCATGTTGATACAGGGGTGTCCATTGGCCGCTGCCAAAGGCCCTCCGATACCA		5700
Db	6290	TACGTCCTCCATGTTGATACAGGGGTGTCCATTGGCCGCTGCCAAAGGCCCTCCGATACCA		6349
Qy	5701	CTCTCAGGAGGAGAGAGAGGTTCCTGTCTAGAAATATACCGATCTTTCGCTTGCGG		5760
Db	6350	CTCTCAGGAGGAGAGAGAGGTTCCTGTCTAGAAATATACCGATCTTTCGCTTGCGG		6409
Qy	5761	GAGCTCGGCACAAAGACCTTCGCGACGCTCCGAATCGTGGCCCTGTGACAGCGCACGCA		5820
Db	6410	GAGCTCGGCACAAAGACCTTCGCGACGCTCCGAATCGTGGCCCTGTGACAGCGCACGCA		5869
Qy	5821	ACGGCTCTCTGTGACAGCCCTCCGAGAGCGCGAGCGGAGATCCGAGTGAATCTGTAC		5880
Db	6470	ACGGCTCTCTGTGACAGCCCTCCGAGAGCGCGAGCGGAGATCCGAGTGAATCTGTAC		6529
Qy	5881	TCTCTCATGSCCCCCCTTTGAGGCGGAGACCGGGGAGATCCCGATCTTCAGCGAGGCTTTGG		5940
Db	6530	TCTCTCATGSCCCCCCTTTGAGGCGGAGACCGGGGAGATCCCGATCTTCAGCGAGGCTTTGG		6589
Qy	5941	TCTACCGTAAACGAGAGAGCTAGTGAAGAGCTGTCTGTCTGTATCTCTTAACATATGG		6000
Db	6590	TCTACCGTAAACGAGAGAGCTAGTGAAGAGCTGTGTCTGTCTGTATCTCTTAACATATGG		6049
Qy	6001	ACAGCGCCCTGATACAGCCATCGCGATGCGCGAGGAACAACGCTCCCATCAATGCAGTG		6060
Db	6650	ACAGCGCCCTGATACAGCCATCGCGATGCGCGAGGAACAACGCTCCCATCAATGCAGTG		6709
Qy	6061	ACCAACTCTTTTGCTCGTACACACACACTTGTATGTACACATCTTCGAGCGGCAAGC		6120
Db	6710	ACCAACTCTTTTGCTCGTACACACACACTTGTATGTACACATCTTCGAGCGGCAAGC		6769
Qy	6121	CTGCGGCGAGAGAGAGTCACTTTGAAGAGCTCAGTCTCTGAGSACACATCCGCGGAG		6180
Db	6770	CTGCGGCGAGAGAGAGTCACTTTGAAGAGCTCAGTCTCTGAGSACACATCCGCGGAG		6829
Qy	6181	GTGCTCAAGGAGATGAAGGCGCAAGGCGCTCCACAGTTAAGGCTTAACCTTCTATCCGTGAG		6240
Db	6830	GTGCTCAAGGAGATGAAGGCGCAAGGCGCTCCACAGTTAAGGCTTAACCTTCTATCCGTGAG		6889
Qy	6241	GAAAGCTGTAAAGCTAGCGCCGCCCATTTGGCGCAGATCTAAATTTTGGCTAATGCGGCAAG		6300
Db	6890	GAAAGCTGTAAAGCTAGCGCCGCCCATTTGGCGCAGATCTAAATTTTGGCGTATGCGGCAAG		6949
Qy	6301	GAGGTCGGGAACCTTTCAGAGAAAGCGGTTAAACACATCCGCTCGCTGTGGAAGACTTG		6360
Db	6950	GAGGTCGGGAACCTTTCAGAGAAAGCGGTTAAACACATCCGCTCGCTGTGGAAGACTTG		7009
Qy	6361	CTGGAAGACACTGAGACACCAATTTGACACACATCATGTGCGAAATAATATAGTCTTTCGCG		6420
Db	7010	CTGGAAGACACTGAGACACCAATTTGACACACATCATGTGCGAAATAATATAGTCTTTCGCG		7069
Qy	6421	GTCGAACCGAGAAAGGGGGGCGAAGCGACGTGGCTTTCGTATTTCCCAATTTGGGG		6480
Db	7070	GTCGAACCGAGAAAGGGGGGCGAAGCGACGTGGCTTTCGTATTTCCCAATTTGGGG		7129
Qy	6481	GTTCTGTGTGGAGAAAAATGGCCCTTACGATGTGCTCACCCCTCCCTCAGGCCGTG		6540

Db	7130	GTTCGTGTGTGGAGAAAATGCCCCCTTTACATGTGTGTCTCCACCCTCCCTCAGGCCGTG	7189
Qy	6541	ATGGGCTCTTCATACGAGATCTCCATATCTCTCTGACAGCGGGTGAAGTTCCCTGSTAT	6600
Db	7190	ATGGGCTCTTCATACGAGATCTCCATATCTCTCTGACAGCGGGTGAAGTTCCCTGSTAT	7249
Qy	6601	GCTTCGAACCGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCGTTTATACCA	6660
Db	7250	GCCGTGAACCGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCGTTTATACCA	7309
Qy	6661	ACGGTCACTGAGATGACATCCGTGTTGAGAGATCATCTACCAATGTTGTGACTTGGCC	6720
Db	7310	ACGGTCACTGAGATGACATCCGTGTTGAGAGATCATCTACCAATGTTGTGACTTGGCC	7369
Qy	6721	CCCGAGCCAGACAGGCCCATAGGTGGCTCACAGACGGGCTTTACATGGGGGGCCCCCTG	6780
Db	7370	CCCGAGCCAGACAGGCCCATAGGTGGCTCACAGACGGGCTTTACATGGGGGGCCCCCTG	7429
Qy	6781	ACTATTTCTAAAGGCGAGAACTCGGCTATCCGCGGTGGCGGCGAGCGGTACTGACG	6840
Db	7430	ACTATTTCTAAAGGCGAGAACTCGGCTATCCGCGGTGGCGGCGAGCGGTACTGACG	7489
Qy	6841	ACCACTGCGGTAAATACCTTCACATGTATTCTTAAGCCCGCTGCGGCTGTGAGCTGGG	6900
Db	7490	ACCACTGCGGTAAATACCTTCACATGTATTCTTAAGCCCGCTGCGGCTGTGAGCTGGG	7549
Qy	6901	AAGTCCAGAGCTCCAGAGATGGCTGATGCGGAGAGAGACACTTGTGCTATCTGTGAAGC	6960
Db	7550	AAGTCCAGAGCTCCAGAGATGGCTGATGCGGAGAGAGACACTTGTGCTATCTGTGAAGC	7609
Qy	6961	GCGGGGAGCCCAAGAGAGAGCGGAGCGCTTACGCGGCTTTCAGAGAGCTATGACTAGATAC	7020
Db	7610	GCGGGGAGCCCAAGAGAGAGCGGAGCGCTTACGCGGCTTTCAGAGAGCTATGACTAGATAC	7669
Qy	7021	TCTGCCCCCTGGGGACCCCGCCCAACCAAGATATGACACTTGGAGTTGATTAACATATGC	7080
Db	7670	TCTGCCCCCTGGGGACCCCGCCCAACCAAGATATGACACTTGGAGTTGATTAACATATGC	7729
Qy	7081	TCTTCCAATGTGTAGTTCGCGCAGATGCATCTGGCAAAAGGCTGTACTATCTCACCCGT	7140
Db	7730	TCTTCCAATGTGTAGTTCGCGCAGATGCATCTGGCAAAAGGCTGTACTATCTCACCCGT	7789
Qy	7141	GACCCACACACCCCTTGGCGGGGTGGCGGAGAGACACTTGACACACTCCAGTCAAT	7200
Db	7790	GACCCACACACCCCTTGGCGGGGTGGCGGAGAGACACTTGACACACTCCAGTCAAT	7849
Qy	7201	TCTTGGCTAGGCAACATCATCATATGCGGCCACCTTGTGGCCAAAGATGATCTGATG	7260
Db	7850	TCTTGGCTAGGCAACATCATCATATGCGGCCACCTTGTGGCCAAAGATGATCTGATG	7909
Qy	7261	ACTCATTTCTTCTCATCTCTCTAGCTCAGGAACAACCTGAAAAAGCCCTAGATTGCA	7320
Db	7910	ACTCATTTCTTCTCATCTCTCTAGCTCAGGAACAACCTGAAAAAGCCCTAGATTGCA	7969
Qy	7321	ATCTACGGGGGCTGTACTTCCATTGAGCAGCACTTACCTACCTAGATCAATTCACGATC	7380
Db	7970	ATCTACGGGGGCTGTACTTCCATTGAGCAGCACTTACCTACCTAGATCAATTCACGATC	8029
Qy	7381	CATGGCCTTAGCGCAATTTTCACTCGATAGTACTCTCCAGTGTGATCATAGGTTGGCT	7440
Db	8030	CATGGCCTTAGCGCAATTTTCACTCGATAGTACTCTCCAGTGTGATCATAGGTTGGCT	8089
Qy	7441	TGATGCGTACGAACTTGGGGTACCGGCTTGGAGTCTGAGACATCGGGCCAGAGT	7500
Db	8090	TGATGCGTACGAACTTGGGGTACCGGCTTGGAGTCTGAGACATCGGGCCAGAGT	8149
Qy	7501	GTTCGCGCTAGGCTACTGTCCAGGGGGGAGAGGCTGGCAATTTGTGGCAATGACTCTTC	7560
Db	8150	GTTCGCGCTAGGCTACTGTCCAGGGGGGAGAGGCTGGCAATTTGTGGCAATGACTCTTC	8209
Qy	7561	AAGTGGCGATGAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGGCTCCCAAGTGGAT	7620
Db	8210	AAGTGGCGATGAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGGCTCCCAAGTGGAT	8269

QY	2	CCAGCCCCGATTGGGGGCGACATCCACATACATACACTCCCTGAGGAGACTACTGT	61	GSISGLGVYLVIADLAGYAGVAGLALFAFKMSSEPMSTEDLAVNLPAJLSIPALWVYV
DB	2	CCAGCCCCGATTGGGGGCGACATCCACATACATACACTCCCTGAGGAGACTACTGT	61	LAARHGVGVADGAYVOMNRRLIAFSRNGEYSPHSEEDAAVATVLIISLTIIO
QY	62	CTTCACGCGAAGAAAGCGCTACAGCATAGGCGTTAGTATGATGTGCTGCACGCTCCACGACC	121	LLRKLHMINIMEDCSTPCSGSMLIPGWDIMCTITLTPFKMLIOMSLKTLPLRPGPFSCOR
DB	62	CTTCACGCGAAGAAAGCGCTACAGCATAGGCGTTAGTATGATGTGCTGCACGCTCCACGACC	121	GKRYKAWGDDIMOTCTPCCAQIITGHKHKMSMLINPGPCSMKSLGTPRIYATVTPGCT
QY	62	CTTCACGCGAAGAAAGCGCTACAGCATAGGCGTTAGTATGATGTGCTGCACGCTCCACGACC	121	PSAPWNSFRALMRVAABEYIVTRVDEDTVTYGTGTTDYVKPCQVPAPEPTEPTGCT
DB	62	CTTCACGCGAAGAAAGCGCTACAGCATAGGCGTTAGTATGATGTGCTGCACGCTCCACGACC	121	LHARAQSPCLLREVEYTFVLGNQYIPVSGQLCEPELELVATLSLTDPSITAEYAK
QY	122	CCCCCTCCCGGGAGAGCCATAGTGGTTCGGGAAACCGGTGAGTACACGGAATTGCGCAG	181	SENVVILDSIEEPLQAEDEREYSPAEILRVSREFPRAMPIMAPDVPNPLEMSWD
DB	122	CCCCCTCCCGGGAGAGCCATAGTGGTTCGGGAAACCGGTGAGTACACGGAATTGCGCAG	181	PENYVAVGCGPLPEAKAPIPPRPKRRIYVLESTVSAALAEATKTFGSESSAVD
QY	122	CCCCCTCCCGGGAGAGCCATAGTGGTTCGGGAAACCGGTGAGTACACGGAATTGCGCAG	181	SGATATSPDSDGDDGSDVESVSMSPLEEDPDITLSDSMSTVSEAESEEDVOC
DB	122	CCCCCTCCCGGGAGAGCCATAGTGGTTCGGGAAACCGGTGAGTACACGGAATTGCGCAG	181	MSATYTGALITTPCAAEETKLPIINALSNLIRHNHLYATTSRSLOROKVTETDRIQ
QY	182	ACGACCGGGGTCTTTCTTGATTCATCAACCCGCTCATATGCTTGAGATTTGGGCGTGGCCCG	241	VLDHYSDKLLIEDETPIIDTTIMAKNEVCYQPEGGRSPALTYLTPGYRVECKMA
DB	182	ACGACCGGGGTCTTTCTTGATTCATCAACCCGCTCATATGCTTGAGATTTGGGCGTGGCCCG	241	NHITSVKDLIEDETPIIDTTIMAKNEVCYQPEGGRSPALTYLTPGYRVECKMA
QY	302	TGCTTGGAGTGGCCCCGGGAGGTCCTGTAAGACCGTGCACCATAGACGAAATCCTTAACC	361	LYDVATSLPOLWMOSSSTGFQYSPGQVRETVLNAWKAKKCPMGFADTDCPSYITEND
DB	302	TGCTTGGAGTGGCCCCGGGAGGTCCTGTAAGACCGTGCACCATAGACGAAATCCTTAACC	361	IRVESITYOCCDLAPEARQAIRSLTRLTGVLIGATLINSKQONQIRCHASCVLTTSCG
QY	362	TCAAGAAACCAAGGAGGCGCGCATGATTGAACAAAGATGATTGACACGAGTTCTCC	421	NTLVQLKAAACRAAKLIDCTMLVCGDLIVGICISAGQDEEASLRFETAMRYSRA
DB	362	TCAAGAAACCAAGGAGGCGCGCATGATTGAACAAAGATGATTGACACGAGTTCTCC	421	PPGPBPPEYDEILITSCGSNVSAVDHAGSKRYVYLTRDPTPLARAMEIARIPVNA
QY	422	GCGCGCTGGGTGGAAGGCTATTGGGCTATGATGCGGCACAAGACAAATGCGTCTCTC	481	SMGINIYATPTLWARMLMTHTFFSILLQEOELKDLQIAGVCSLEPDLQIIO
DB	422	GCGCGCTGGGTGGAAGGCTATTGGGCTATGATGCGGCACAAGACAAATGCGTCTCTC	481	RHLGHSASFSLHSYSPGEINRWASCLRLKRGPLPVRVHRHARSVARRLLSOGRAATCG
QY	482	TGATGCGCGCGGTTCCTCGGCTGTCAAGCGAGGCGCCCGGTTCTTTTGTCAAGACGA	541	KYLINMAVRTKLITPIIPASQDLDSLSEFVAGSGGDIYHSLSRRAPPMFMWLLLSL
DB	482	TGATGCGCGCGGTTCCTCGGCTGTCAAGCGAGGCGCCCGGTTCTTTTGTCAAGACGA	541	VVGCIYLLPNR"
QY	542	CTGTCCGCGTGGCCCTAATGAAGTGTAGAGACAGGACAGGCGGTATCGTGGGCGCAC	601	
DB	542	CTGTCCGCGTGGCCCTAATGAAGTGTAGAGACAGGACAGGCGGTATCGTGGGCGCAC	601	
QY	602	GACGGGCGTTCTTGCGACAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGAGCTGCT	661	
DB	602	GACGGGCGTTCTTGCGACAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGAGCTGCT	661	
QY	662	GCTATTGGGGAAGTCCGGGAGAGATTCCTGTCAATCTACCTTGTCTCGCGAGAA	721	

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Db 662 GCTATTGGGGAAGTCCGGGAGAGATCTCTGTCACTACCTTCTCTCCGCGAAG 721
QY 722 AGTATCCATCATGGCTGATGATGATGCGGCGGCTGCATACGCTTATCCGATACCTCC 781
Db 722 AGTATCCATCATGGCTGATGATGATGCGGCGGCTGCATACGCTTATCCGATACCTCC 781
QY 782 ATTGCACCCCAAGCAAAACATCGCATGAGGAGACACTACTGGATGGAAGCGGCT 841
Db 782 ATTGCACCCCAAGCAAAACATCGCATGAGGAGACACTACTGGATGGAAGCGGCT 841
QY 842 TGTGATCAAGGATGATGAGAGAGATCAGGGGCTCCGCGCAGCCGAAGCTGTTGCG 901
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QY 902 CAGGCTCAAGGCGCGATCCCGAGGAGAGATCTGCTGATGCCATGGCATGCTG 961
Db 902 CAGGCTCAAGGCGCGATCCCGAGGAGAGATCTGCTGATGCCATGGCATGCTG 961
QY 962 CTTCGCAATATCATGATGATGGAATGCGCGCTTTCTGATTCATGCACTGTGCGCGCT 1021
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Db 1142 GCGCATCGCTTATATGCGCTTCTTGACGAGTCTTCTGAGT-----TAAC 1189
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QY 1611 AAGAGTCAATGGCTCTCTCAAGAGTATTAACAAGGGCTGAAGATGCCAGAGG 1670
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Db 1731 CGAGGTTAAAAACGTTAGGCGCCCGGACACAGGAGAGTGTGTTTCTTTAAAAAC 1790
QY 1790 AAGATATATCCATG----- 1803
Db 1791 AAGATATATCCATGAGGAGAGAGATGAGAGATGAGAGATGAGAGAGGCTTGTAGCTC 1850
QY 1804 ----- 1803
Db 1851 TGAATCTTGTACCTTGTACACCGCATATAGCTGTTCTCTGCTAGAGCTCATATGCTGT 1910
QY 1804 ----- 1803
Db 1911 TACAATATTTATACAGGAGGAGGAGACACTTGCAGAGTGTGATCCCCCCTCAAG 1970
QY 1804 ----- 1803
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QY 1804 ----- 1803
Db 2031 TTACATACCAAAATCTGTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2090
QY 1804 ----- 1803
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QY 1804 ----- 1803
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QY 1804 ----- 1803
Db 2211 GTACGTACCTTATGATACCATCTACCCACTGCGGAGCTGAGGCCACGCGGCTGAGAG 2270
QY 1804 ----- 1803
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QY 1804 ----- 1803
Db 2331 GGGGAGCAGACCGCGGCTGTGGGACATCATCTTGGGCTGCGCGCTCCCGCCGCA 2390
QY 1804 ----- 1803
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QY 1804 ----- 1803
Db 2451 TCGGCTTATGAGGCTTACTCCCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2510
QY 1862 GCTTCACAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1921
Db 2511 GCTTCACAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2570
QY 1922 CACATCTTCTCTGCGCAACCTGCTCAATGAGGCTGCTGAGTGTGATGATGAGGAGG 1981
Db 2571 CACATCTTCTCTGCGCAACCTGCTCAATGAGGCTGCTGAGTGTGATGATGAGGAGG 2630
QY 1982 GCTCAAGACCTTCCGCGCCCAAGAGGCGCAATCAACCAATGTAACCAATGTGAGAC 2041
Db 2631 GCTCAAGACCTTCCGCGCCCAAGAGGCGCAATCAACCAATGTAACCAATGTGAGAC 2690
QY 2042 AGGACCTGCTGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2101
Db 2691 AGGACCTGCTGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2750
QY 2102 GCAGCTGAGCTTACTTGTGTCAGAGGAGTCCGATGTCATTCGAGTCCGCGCGG 2161
Db 2751 GCAGCTGAGCTTACTTGTGTCAGAGGAGTCCGATGTCATTCGAGTCCGCGCGG 2810
QY 2162 GCGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2221
Db 2811 GCGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2870

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QY	2222	GCCTCCACAGCCTCTGCCCCCTGGGGGACAGCTGTTGGGATATCTTCGGGGCTGCCGTGTGA	2281
Db	2871	GGGGTCCACTGCTCTGCCCCCTGGGGGACAGCTGTGGGATATCTTCGGGGCTGCCGTGTGA	2930
QY	2282	CCCGAGGGGGTGTGGAAAGGGCGGTGACCTTGTATACCGCTGCACTCTATGTGGAAACCACTATGC	2341
Db	2931	CCCGAGGGGGTGTGGAAAGGGCGGTGACCTTGTATACCGCTGCACTCTATGTGGAAACCACTATGC	2990
QY	2342	GGTCCCCGGGCTTCACAGACACTGTGCCCCCTGGGGCGCTACGGCACAATTCAGATG	2401
Db	2991	GGTCCCCGGGCTTCACAGACACTGTGCCCCCTGGGGCGCTACGGCACAATTCAGATG	3050
QY	2402	CCCATCTACACGCCCCCTACTGTGTAGCGGCAAGAGCACTAAGTGTCCGGCTGCGTATGCA	2461
Db	3051	CCCATCTACACGCCCCCTACTGTGTAGCGGCAAGAGCACTAAGTGTCCGGCTGCGTATGCA	3110
QY	2462	CCCAAGGGTATAGTGGCTGTGCTGCTGGAACCCGTGCGTGGCGGCAACCTTAGTTGGGG	2521
Db	3111	CCCAAGGGTATAGTGGCTGTGCTGCTGGAACCCGTGCGTGGCGGCAACCTTAGTTGGGG	3170
QY	2522	CGTATATGTTAAGGCATGTGATGACCCCTAATCATGAGAACCGGGGTAAAGACATCA	2581
Db	3171	CGTATATGTTAAGGCATGTGATGACCCCTAATCATGAGAACCGGGGTAAAGACATCA	3230
QY	2582	CCAGGGTGGCCCATACAGTACTGCACCTATGCAAGTTCTTGCGAGCGTGGTGTCT	2641
Db	3231	CCAGGGTGGCCCATACAGTACTGCACCTATGCAAGTTCTTGCGAGCGTGGTGTCT	3290
QY	2642	CTGGGGGCGCCTATGACATCATATATATGTATGATGAGTGTGCACATGACTGTGACACATTA	2701
Db	3291	CTGGGGGCGCCTATGACATCATATATGTATGATGAGTGTGCACATGACTGTGACACATTA	3350
QY	2702	TTCGGGGCATACGGCAAGTCTGGGACCAAGCGGAGACGGCTGGAGCGGATGTGCTGTC	2761
Db	3351	TTCGGGGCATACGGCAAGTCTGGGACCAAGCGGAGACGGCTGGAGCGGATGTGCTGTC	3410
QY	2762	TCCGCACCGCTAGCGCTCCGGGATCGGTACCGCTCCCATCCATCCAAATCGAGAGGTGG	2821
Db	3411	TCCGCACCGCTAGCGCTCCGGGATCGGTACCGCTCCCATCCAAATCGAGAGGTGG	3470
QY	2822	CTCTGTCACAGACATGGAGAAATCCCTTTTATGGCAAGCCATCCCTCTCGACACATCA	2881
Db	3471	CTCTGTCACAGACATGGAGAAATCCCTTTTATGGCAAGCCATCCCTCTCGACACATCA	3530
QY	2882	AGGGGGGAGGACACCTCATTTTCTGCCATTCCAAGAGAATGTGATGAGCTGCCCGGA	2941
Db	3531	AGGGGGGAGGACACCTCATTTTCTGCCATTCCAAGAGAATGTGATGAGCTGCCCGGA	3590
QY	2942	AGCTGTCCGGGCTGGGACATAATGTGTGACATATTATACCGGGGCTTGATGTATACGTCA	3001
Db	3591	AGCTGTCCGGGCTGGGACATAATGTGTGACATATTATACCGGGGCTTGATGTATACGTCA	3650
QY	3002	TACCAACTAGCGAGACGTATTTGTGTAGACAAGAGCGCTCTAATGACGGGCTTTTACCG	3061
Db	3651	TACCAACTAGCGAGACGTATTTGTGTAGACAAGAGCGCTCTAATGACGGGCTTTTACCG	3710
QY	3062	GCATTTTGACTCTAGTATGACTGTGCAATTCATATGTGTACCCAGACAGTCGACTCAAGC	3121
Db	3711	GCATTTTGACTCTAGTATGACTGTGCAATTCATATGTGTACCCAGACAGTCGACTCAAGC	3770
QY	3122	TGGACCCGACTTACCATTTGAGACGACGACGTGCAACAGACGGGTGTACGCTGC	3181
Db	3771	TGGACCCGACTTACCATTTGAGACGACGACGTGCAACAGACGGGTGTACGCTGC	3830
QY	3182	AGCGCCAGGAGAGACATGTAAGGGGCGAGATGGGCAATTAACAGTTTGTGATCCAGAG	3241
Db	3831	AGCGCCAGGAGAGACATGTAAGGGGCGAGATGGGCAATTAACAGTTTGTGATCCAGAG	3890
QY	3242	AACGGCCCTCGGGCATGTTGCAATTCCTCGSTTCTGTGCAGTGTATGACGCGGGCTGTG	3301
Dh	3891	AACGGCCCTCGGGCATGTTGCAATTCCTCGSTTCTGTGCAGTGTATGACGCGGGCTGTG	3950

QY	3302	CTTGTCAGAGCTCACGCCGCCGAGACCTCAGTTAGTTGCGGGCTTACTTAACACAC	3361
Db	3951	CTTGTCAGAGCTCACGCCGCCGAGACCTCAGTTAGTTGCGGGCTTACTTAACACAC	4010
QY	3362	CAGGGTTCGCCGCTCCAGAGACATCTGSAATTCTGGGAGAGGGTCTTTACAGGGCTCA	3421
Db	4011	CAGGGTTCGCCGCTCCAGAGACATCTGSAATTCTGGGAGAGGGTCTTTACAGGGCTCA	4070
QY	3422	CCCACTAGACGCCCATTTCTTGTGCCAGACTAACAGGACAGAGACACTTCCCTAC	3481
Db	4071	CCCACTAGACGCCCATTTCTTGTGCCAGACTAACAGGAGAGACACTTCCCTAC	4130
QY	3482	TGGTAGCATACCAAGGCTACGGTGTGGCGCAGGGCTCAGGCTCCACTTCGTGGAGCC	3541
Db	4131	TGGTAGCATACCAAGGCTACGGTGTGGCGCAGGGCTCAGGCTCCACTTCGTGGAGCC	4190
QY	3542	AAATGTGGAGTGTCTCATACGGCTTAACCCCTACGCTGACGGGGCAAGGCCCTGTGT	3601
Db	4191	AAATGTGGAGTGTCTCATACGGCTTAACCCCTACGCTGACGGGGCAAGGCCCTGTGT	4250
QY	3602	ATAGGCTGGGAGCCGTTCAAAAGAGGTTACTACCAACACCCTAACAATATCATCA	3661
Db	4251	ATAGGCTGGGAGCCGTTCAAAAGAGGTTACTACCAACACCCTAACAATATCATCA	4310
QY	3662	TGGCATCATGTGGGGCTGACCTGGAGGGTGTCACGACACGCTGGGTGGTAGAGGAG	3721
Db	4311	TGGCATCATGTGGGGCTGACCTGGAGGGTGTCACGACACGCTGGGTGGTAGAGGAG	4370
QY	3722	TCTTAGCAGCTCTGGCCGCGCTATTGCTGACACAAGCAGCGTGTCTATTGTGGCGAGA	3781
Db	4371	TCTTAGCAGCTCTGGCCGCGCTATTGCTGACACAAGCAGCGTGTCTATTGTGGCGAGA	4430
QY	3782	TCATCTGTCCGGAGGCGCGCCCATCATCCGACAGGAACTCTTTACGGGAGTTGC	3841
Db	4431	TCATCTGTCCGGAGGCGCGCCCATCATTCGCCAGAGGAATCTTTACGGGAGTTGC	4490
QY	3842	ATGAGATGGAAGAGTGCGCCTCAACCTCCCTTACATGACAGGAATGACGTCCGC	3901
Db	4491	ATGAGATGGAAGAGTGCCTCTCACACCTCCTTACATGACAGGAATGACAGCTCCGC	4550
QY	3902	AACATTTCAACACAGAAGGCAATCGGGTGTGTGAACACGCCACCAAGACAGCGAGGCTG	3961
Db	4551	AACATTTCAACACAGAAGGCAATGGGGTGTGTGAACACGCCACCAAGACAGCGAGGCTG	4610
QY	3962	CTGCTCCCGGTGGTAATCCAAGTGGCGGACCTCGAAGCTTTCTGGGCGAAGCATATGT	4021
Db	4611	CTGCTCCCGGTGGTAATCCAAGTGGCGGACCTCGAAGCTTTCTGGGCGAAGCATATGT	4670
QY	4022	GGAATTTATAGCGGGAGTACAATATTATACAGGCTTGTCACCTGTGCTGGCAACCCCG	4081
Db	4671	GGAATTTATAGCGGGAGTACAATATTATACAGGCTTGTCACCTGTGCTGGCAACCCCG	4730
QY	4082	CGATAGCATCACTGATGAGCATTCAGACGCTCTATCACAGCGCGGTCAACACCAACATTA	4141
Db	4731	CGATAGCATCACTGATGAGCATTCAGACGCTCTATCACAGCGCGGTCAACACCAACATTA	4790
QY	4142	CCCTCCTATTACATCTCGGGGGAGTGGGTGGCCGCCCAACTTGTCTCTCCACGCGTG	4201
Db	4791	CCCTCCTATTACATCTCGGGGGAGTGGGTGGCCGCCCAACTTGTCTCTCCACGCGTG	4850
QY	4202	CTTCTGCTTTTGTAGGGCGCGCATGCGTGTGAGACGGCTGTGGCACATAGGCGCTTTGGGA	4261
Db	4851	CTTCTGCTTTTGTAGGGCGCGCATGCGTGTGAGACGGCTGTGGCACATAGGCGCTTTGGGA	4910
QY	4262	AGGTCTTGAGGATATTTTGGCAGGTTATGAGACAGGGGTGGGAGCGCGCTGTGGGCT	4321
Db	4911	AGGTCTTGAGGATATTTTGGCAGGTTATGAGACAGGGGTGGGAGCGCGCTGTGGGCT	4970
QY	4322	TTAAGGTATAGGCGGCGAGATGCGCTTCACACGAGACCTGSGTAACTACTACTCCCTGCTA	4381
Db	4971	TTAAGGTATAGGCGGCGAGATGCGCTTCACACGAGACCTGSGTAACTACTACTCCCTGCTA	5030
QY	4382	TCCTCTCCCGTGGGCGCCCTACTCTCGGGGTGTGTGCCAGGATATGCTGTGGCAGC	4441

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OY 4562 AGATCCCTCTAGTCTTACATCACTAGCTGTGAAGAGGCTTCCACAGTGAATCAAG 4621
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OY 5942 CTACCGTAAAGGAGAGGCTAGTGAAGACCTGCTGCTGCTGATGCTCTACACATGA 6001
Db 6591 CTACCGTAAAGGAGAGGCTAGTGAAGACCTGCTGCTGCTGATGCTCTACACATGA 6650
OY 6002 CAGGCGCTGATACGCGCATGCGCTCGGAGGAAACCAAGCTGCCATTAATGCACTGA 6061
Db 6651 CAGGCGCTGATACGCGCATGCGCTCGGAGGAAACCAAGCTGCCATTAATGCACTGA 6710
OY 6062 GCAATCTTGTCTCGTCCAGCACAACTGGTCTAGTCTACACATCTCCGAGCGCAAGCC 6121
Db 6711 GCAATCTTGTCTCGTCCAGCACAACTGGTCTAGTCTACACATCTCCGAGCGCAAGCC 6770
OY 6122 TGGGCGAGAGAGGTCACCTTTGACAGACTGCGAGTCTGGACAGCACTACCGGAGG 6181
Db 6771 TGGGCGAGAGAGGTCACCTTTGACAGACTGCGAGTCTGGACAGCACTACCGGAGG 6630
OY 6182 TGCTCAAGAGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGAGG 6241
Db 6631 TGCTCAAGAGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGAGG 6890
OY 6242 AAGCTGTAGTGAAGCGCCCGACATTCGGCGAGATCTAAATTTGGCTATGGGCAAGG 6301
Db 6891 AAGCTGTAGTGAAGCGCCCGACATTCGGCGAGATCTAAATTTGGCTATGGGCAAGG 6950
OY 6302 AAGTCCGGAACCTATCCAGCAAGGCGTAAACCAATCCGCTCCGTGGAAGGACTTGC 6361
Db 6951 AAGTCCGGAACCTATCCAGCAAGGCGTAAACCAATCCGCTCCGTGGAAGGACTTGC 7010
OY 6362 TGAAGACACTGAGACACCAATTGACACCAACCATATGCAAAAAATGAGGTTTCTGCG 6421
Db 7011 TGAAGACACTGAGACACCAANTTGAACCAACCATATGCAAAAAATGAGGTTTCTGCG 7070
OY 6422 TCCAACAGAGAGAGGGGCGCAAGCCAGCTCGCTTATGTATTCACAGATTTGGGGG 6481
Db 7071 TCCAACAGAGAGAGGGGCGCAAGCCAGCTCGCTTATGTATTCACAGATTTGGGGG 7130
OY 6482 TTGCTGTGCGAGAAATGAGGCTTTAGAGTGTGTGCTCCACCCCTCCCTAGGCGGTGA 6541
Db 7131 TTGCTGTGCGAGAAATGAGGCTTTAGAGTGTGTGCTCCACCCCTCCCTAGGCGGTGA 7190
OY 6542 TGGGCTCTTCATACGAGTTCATATCTCTCTGAGACAGGGGTGAGGTTCTCTGGTGAATG 6601
Db 7191 TGGGCTCTTCATACGAGTTCATATCTCTCTGAGACAGGGGTGAGGTTCTCTGGTGAATG 7250
|||||

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QY 6602 CCTGAAGCGAAGAAATGCCCTATGAGGCTTCGATATGACACCGCGTGTGACTCAA 6661
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Db 7251 CCGGAAGGAGAAATGCCCTATGAGGCTTCGATATGACACCGCGTGTGACTCAA 7310
6662 CGGTCTAGAGATGACATCCGTTGAGAGTCAATCTACCAATGTTGTACTTGGCC 6721
Db 7311 CGGTCTAGAGATGACATCCGTTGAGAGTCAATCTACCAATGTTGTACTTGGCC 7370
QY 6722 CCGAAGCGAAGCGCATAGGTGCGTACAGAGCGGCTTTACATCGGGGGCCCCGGA 6781
Db 7371 CCGAAGCGAAGCGCATAGGTGCGTACAGAGCGGCTTTACATCGGGGGCCCCGGA 7430
QY 6782 CTAATCTAAAGGGCAGAACTCGGCTATCGCGGTGCCGGCAGCGGTGTACTGAGA 6841
Db 7431 CTAATCTAAAGGGCAGAACTCGGCTATCGCGGTGCCGGCAGCGGTGTACTGAGA 7490
QY 6842 CCAAGTGGGTAAATACCTCACATGTTACTTGAAGCGCGTTCGCGCTGTGAGAGTGA 6901
Db 7491 CCAAGTGGGTAAATACCTCACATGTTACTTGAAGCGCGTTCGCGCTGTGAGAGTGA 7550
QY 6902 AGCTCCAGAGCTCCAGATGCTGTAATGCGGAGAGACGCTTGTCTGTGAAGCG 6961
Db 7551 AGCTCCAGAGCTCCAGATGCTGTAATGCGGAGAGACGCTTGTCTGTGAAGCG 7610
QY 6962 CCGGAGACCCAGAGAGACGAGGCGAGGCTTCACGAGAGGCTATGACTATGACT 7021
Db 7611 CCGGAGACCCAGAGAGACGAGGCGAGGCTTCACGAGAGGCTATGACTATGACT 7670
QY 7022 CTGCCCCCTGGGGAGCCGCCCAACAGAAATAGACTTGGAGTTGATTAACATCATCT 7081
Db 7671 CTGCCCCCTGGGGAGCCGCCCAACAGAAATAGACTTGGAGTTGATTAACATCATCT 7730
QY 7082 CCTTCGAATGTGTAGTGGGCAAGATGCAATGCGCAAAAGGTTACTATCTCACCCGTG 7141
Db 7731 CCTTCGAATGTGTAGTGGGCAAGATGCAATGCGCAAAAGGTTACTATCTCACCCGTG 7790
QY 7142 ACCCGACACCCCTTGGCGGGGCTGCGTGGGAGACGCTAGACACTCCAGTCAATT 7201
Db 7791 ACCCGACACCCCTTGGCGGGGCTGCGTGGGAGACGCTAGACACTCCAGTCAATT 7850
QY 7202 CCTGGCTAGGCAACATCATATGATATGCGCCCACTTGGGCAAGATGATCTGATGA 7261
Db 7851 CCTGGCTAGGCAACATCATATGATATGCGCCCACTTGGGCAAGATGATCTGATGA 7910
QY 7262 CTGATTTCTTCTCATCTCTCTAGCTCAGGAACTTGAAGAGCCCTAGATTGTGAGA 7321
Db 7911 CTGATTTCTTCTCATCTCTCTAGCTCAGGAACTTGAAGAGCCCTAGATTGTGAGA 7970
QY 7322 TCTACGGGGGCTGTACTCCATTGAGCACTTGACCTACCTCAGATCAATCAAGACTCC 7381
Db 7971 TCTACGGGGGCTGTACTCCATTGAGCACTTGACCTACCTCAGATCAATCAAGACTCC 8030
QY 7382 ATGGCCCTTAGGCAATTTTCACTCATAGTTACTCTCCAGGTAGATCAATAGGATGGCT 7441
Db 8031 ATGGCCCTTAGGCAATTTTCACTCATAGTTACTCTCCAGGTAGATCAATAGGATGGCT 8090
QY 7442 CATGCCCTCAGGAAACTTGGGGTACGCCCTTGGGAGTCTGGAGACATCGGGCCAGAAGTG 7501
Db 8091 CATGCCCTCAGGAAACTTGGGGTACGCCCTTGGGAGTCTGGAGACATCGGGCCAGAAGTG 8150
QY 7502 TCCGGGCTAGGCTACTGTGCCAGGGGGGAGGGGCTGCCACTGTGGCAAGTACCTCTCA 7561
Db 8151 TCCGGGCTAGGCTACTGTGCCAGGGGGGAGGGGCTGCCACTGTGGCAAGTACCTCTCA 8210
QY 7562 ACTGGGAGTAAAGACCAAGCTCAAACTCACTCCAACTCCGGCTGCTCCAGTTGATT 7621
Db 8211 ACTGGGAGTAAAGACCAAGCTCAAACTCACTCCAACTCCGGCTGCTCCAGTTGATT 8270
QY 7622 TATCCAGTGTGCTGCTGCTGCTTACAGGGGGGAGACATATATCACAGCTGTCTGCTG 7681
Db 8271 TATCCAGTGTGCTGCTGCTGCTTACAGGGGGGAGACATATATCACAGCTGTCTGCTG 8330

QY 7682 CCCGACCCCGCTGCTTCAATGAGTGGCTACTTCTCTGTAAGGGGTAGGCATCTATC 7741
|||||
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QY 7742 TACTCCCAACGATGAGACGGGAGCTTAACACTCCAGGCCAATAGGCATCTCTTTT 7801
Db 8391 TACTCCCAACGATGAGACGGGAGCTTAACACTCCAGGCCAATAGGCATCTCTTTT 8450
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Db 8451 TTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8510
QY 7862 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7921
Db 8511 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8570
QY 7922 AGCTGGAAGGTCCGTGAGCCGCTTGACTGAGAGAGTGTGATCTAGGCTCTGCA 7981
Db 8571 AGCTGGAAGGTCCGTGAGCCGCTTGACTGAGAGAGTGTGATCTAGGCTCTGCA 8630
QY 7982 GATCAAGT 7989
Db 8631 GATCAAGT 8638

Search completed: May 31, 2003, 12:05:03
Job time : 13261 secs

XX Blichko V;
XX
DR WPI: 2002-490082/52.
DR P-PSDB: AAO18000, AAO18001.
XX
XX Novel nucleic acid encoding replication competent recombinant hepatitis
PT C virus genome useful for screening anti-hepatitis C virus therapeutics
PT and for vaccine development -
XX
PS Claim 6: Page 43-47; 85pp; English.
XX
XX The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement
CC non-infectious, replication-defective infection-component, and
CC replication-defective non-infectious HCV, in gene therapy or gene
CC vaccination targeted to hepatic tissue for treating an animal infected or
CC susceptible to HCV infection and for studying HCV infection and
CC propagation. The present sequence is a clone of a fragment of the HCV
CC genome which encodes the core-neo and NS3 proteinase/helicase proteins.
XX
XX Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 other;
XX

Query Match 99.9%; Score 7985.6; DB 24; Length 7992;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCAGCCCCGATGGGGGCGACACTCCACCTATGATCTCTCCCTGGAGAACTACTG 60
DB 1 GCCAGCCCCGATGGGGGCGACACTCCACCTATGATCTCTCCCTGGAGAACTACTG 60
QY 61 TCTTCAAGCAGAAAGCGTTAGCCATGCGTTAGTATGATGTCGTCAGCCCTCCAGAGAC 120
DB 61 TCTTCAAGCAGAAAGCGTTAGCCATGCGTTAGTATGATGTCGTCAGCCCTCCAGAGAC 120
QY 121 CCCCCCTCCCGSAGAGACCATAGTGTGTGCGGAACCGGTGACTACACCGGAATTGGCAG 180
DB 121 CCCCCCTCCCGSAGAGACCATAGTGTGTGCGGAACCGGTGACTACACCGGAATTGGCAG 180
QY 121 CCCCCCTCCCGSAGAGACCATAGTGTGTGCGGAACCGGTGACTACACCGGAATTGGCAG 180
DB 121 CCCCCCTCCCGSAGAGACCATAGTGTGTGCGGAACCGGTGACTACACCGGAATTGGCAG 180
QY 181 GAGACCGGGTCTTCTTCTTGATCAACCCGCTCAATGCTGAGATTTGGGGCTGCCCC 240
DB 181 GAGACCGGGTCTTCTTCTTGATCAACCCGCTCAATGCTGAGATTTGGGGCTGCCCC 240
QY 241 GCGAGACTGCTAGCCAGTAGTGTGTGCGGAAAGCGTTGTGTACTGCTGATAGG 300
DB 241 GCGAGACTGCTAGCCAGTAGTGTGTGCGGAAAGCGTTGTGTACTGCTGATAGG 300
QY 301 GTGCTTCCGAGTCCCGGGAGGTCTGTAAGCCGTGACCATGAGCAGCAATCTTAAC 360
DB 301 GTGCTTCCGAGTCCCGGGAGGTCTGTAAGCCGTGACCATGAGCAGCAATCTTAAC 360
QY 361 CTCAGAGAAACCAAGAGGCGCCATGATGAAACAGATGATGCAACGAGGTTCTC 420
DB 361 CTCAGAGAAACCAAGAGGCGCCATGATGAAACAGATGATGCAACGAGGTTCTC 420
QY 421 CGGCGCTTGGTGGAGAGGCTATGCGCTATGACTGGGACACAGCAATCGGCTGCT 480
DB 421 CGGCGCTTGGTGGAGAGGCTATGCGCTATGACTGGGACACAGCAATCGGCTGCT 480
QY 481 CTGATGCGCGCGTGTCTCCGCTGTCAAGCGAGGGCGCCGGTCTTTTGTCAAGACCG 540
DB 481 CTGATGCGCGCGTGTCTCCGCTGTCAAGCGAGGGCGCCGGTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGCTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 541 ACCTGTCCGCTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 601 CGACGGGGCTTCTTCCGACAGTGTGCTGACGCTTGTACTGAGCGGGAAGGAGTGGC 660
DB 601 CGACGGGGCTTCTTCCGACAGTGTGCTGACGCTTGTACTGAGCGGGAAGGAGTGGC 660
QY 661 TGGTATTTGGGGAAAGTGGCGGGGGAGGATGCTCTGATCATGCACTTGTCTGCGGAGA 720
DB 661 TGGTATTTGGGGAAAGTGGCGGGGGAGGATGCTCTGATCATGCACTTGTCTGCGGAGA 720
QY 721 AAGTATTCATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 AAGTATTCATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 CATTGACACCAACCAAGCAATCCGATCGAGCGAGCAACGATGATGATGATGATGATG 840
DB 781 CATTGACACCAACCAAGCAATCCGATCGAGCGAGCAACGATGATGATGATGATGATG 840
QY 841 TTGTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 841 TTGTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 901 CCAGGCTCAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
DB 901 CCAGGCTCAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 961 GCTTGCAGATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 GCTTGCAGATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 TGGGTGTGGCGGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 TGGGTGTGGCGGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 TTGGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 TTGGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 AGCGATGCGCTTATGCGCTTCTTGTGAGAGTCTTGTGAGTTTAAACACCAACAGC 1200
DB 1141 AGCGATGCGCTTATGCGCTTCTTGTGAGAGTCTTGTGAGTTTAAACACCAACAGC 1200
QY 1201 GTTTCCTCTAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 GTTTCCTCTAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 CGAAGCGGCTTGAATTAAGGCGGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 CGAAGCGGCTTGAATTAAGGCGGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 CCGTCTTTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 CCGTCTTTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 AGGGGCTTCTTCCCTCTCCCAAGGAATGCAAGGTCTGTTGAATGTGCTGAAGAGCA 1440
DB 1381 AGGGGCTTCTTCCCTCTCCCAAGGAATGCAAGGTCTGTTGAATGTGCTGAAGAGCA 1440
QY 1441 GTTTCCTCTGGAACCTCTTGAAGAGCAACAGCTGATGATGATGATGATGATGATG 1500
DB 1441 GTTTCCTCTGGAACCTCTTGAAGAGCAACAGCTGATGATGATGATGATGATGATG 1500
QY 1501 AACCCCGACCTGCGAGAGGTGCTCTGCGGCCAAAAGCCACGTTAAGATACACCT 1560
DB 1501 AACCCCGACCTGCGAGAGGTGCTCTGCGGCCAAAAGCCACGTTAAGATACACCT 1560
QY 1561 GCAAGGCGGCAACACCCAGTGCACGTTGAGATGATGATGATGATGATGATGATGATG 1620
DB 1561 GCAAGGCGGCAACACCCAGTGCACGTTGAGATGATGATGATGATGATGATGATGATG 1620
QY 1621 TGGCTCTCTCAAGCGTATTCACAGAGGCTGAAGAGTCCAGAGGATACCCATTGT 1680
DB 1621 TGGCTCTCTCAAGCGTATTCACAGAGGCTGAAGAGTCCAGAGGATACCCATTGT 1680
QY 1681 ATGGGATCTATCTGGGGCTCGGTCGACATGCTTACATGTGTTAGTCGAGGTTAAA 1740

Db	1681	ATGGGATCTGATGTGGGGCTTGTCACATGCTTTACATGTGTTAGTGAGGTTAAAA	1740
QY	1741	AAGGTATAGCCCCCGAACAACAGGGGAGTGGTTTTCTTTGAAAAACGATTAATACC	1800
Db	1741	AAGGTATAGCCCCCGAACAACAGGGGAGTGGTTTTCTTTGAAAAACGATTAATACC	1800
QY	1801	ATGGCGGCTATTACGGGCTACACCAACAAGACGGAGGCGTACTTGGCTCATCATCAGT	1860
Db	1801	ATGGCGGCTATTACGGGCTACTGCCAACAGACGGAGGCGTACTTGGCTCATCATCAGT	1860
QY	1861	AGCCTCAAGCCGGGAGACAGAACAGGTGAGGGGAGTCCAGAGTGTCTCCACGCA	1920
Db	1861	AGCCTCAAGCCGGGAGACAGAACAGGTGAGGGGAGTCCAGAGTGTCTCCACGCA	1920
QY	1921	ACAAATCTTCTGGCGACGTGCGCAATGGCGGTGTGTGACGTGCTATCATAGTGC	1980
Db	1921	ACAAATCTTCTGTGGCGACGTGCGCAATGGCGGTGTGTGACGTGCTATCATAGTGC	1980
QY	1981	GGCTCAAGAACCCTTGCCGGCCCAAGGGCCCAATCACCCAATGTACCATGTGAGC	2040
Db	1981	GGCTCAAGAACCCTTGCCGGCCCAAGGGCCCAATCACCCAATGTACCATGTGAGC	2040
QY	2041	CAGGACCTGTGAGGTGGCAAGGGCCCCGGGGGGCGCTTCCTTGACACCATGACCTGC	2100
Db	2041	CAGGACCTGTGCGGTGGCAAGGGCCCCGGGGGGCGCTTCCTTGACACCATGACCTGC	2100
QY	2101	GGCAGCTCGGACCTTTACTTGTGTACAGAGCAATGCCGATGTCAATTCGGTGC	2160
Db	2101	GGCAGCTCGGACCTTTACTTGTGTACAGAGCAATGCCGATGTCAATTCGGTGC	2160
QY	2161	GGCAGCAGCAGGGGGAGCCCTACTCTCCCCAGGCCGATCCCTACTTAAAGGCTCTCG	2220
Db	2161	GGCAGCAGCAGGGGGAGCCCTACTCTCCCCAGGCCGATCCCTACTTAAAGGCTCTCG	2220
QY	2221	GGCGGTCCACTGCTCTGCCCCCTCGGGGCAAGCTGTGAGCATCTTTGGGGTGC	2280
Db	2221	GGCGGTCCACTGCTCTGCCCCCTCGGGGCAAGCTGTGAGCATCTTTGGGGTGC	2280
QY	2281	ACCCGAGGGGTGTGAAGGGGTGTGACTTTGTAACCGGTGAGATCATGGAACCATATG	2340
Db	2281	ACCCGAGGGGTGTGAAGGGGTGTGACTTTGTAACCGGTGAGATCATGGAACCATATG	2340
QY	2341	CGGTCCCGGCTTCAAGGACAATGTGCCCTCGGGCGTACCCGACATTCGCAAGTG	2400
Db	2341	CGGTCCCGGCTTCAAGGACAATGTGCCCTCGGGCGTACCCGACATTCGCAAGTG	2400
QY	2401	GCCCATCTACACGACCCCTACTGTGTAGCGGCAAGAGCACTAAAGTCCCGCTATGCA	2460
Db	2401	GCCCATCTACACGACCCCTACTGTGTAGCGGCAAGAGCACTAAAGTCCCGCTATGCA	2460
QY	2461	GCCCAAGGTTAAGGTGCTTGTTCCTGTAACCGGTGCCGTGCCGCAACCTAGTTGGG	2520
Db	2461	GCCCAAGGTTAAGGTGCTTGTTCCTGTAACCGGTGCCGTGCCGCAACCTAGTTGGG	2520
QY	2521	GGGTATGTGTTAAGGACATGTGATCGAACCTCAACATAGAACCGGGTAAAGCAATC	2580
Db	2521	GGGTATGTGTTAAGGACATGTGATCGAACCTCAACATAGAACCGGGTAAAGCAATC	2580
QY	2581	ACCACGGTGCCTCCCATCAGTACTCCACTATGCAAGTCTTCTGCGAGGGTGTTCG	2640
Db	2581	ACCACGGTGCCTCCCATCAGTACTCCACTATGCAAGTCTTCTGCGAGGGTGTTCG	2640
QY	2641	TCTGGGGCGCCTATGACATCATTAATGTGATGAGTGCACCTCAACTGACTCGACACT	2700
Db	2641	TCTGGGGCGCCTATGACATCATTAATGTGATGAGTGCACCTCAACTGACTCGACACT	2700
QY	2701	ATCTGGGCGATCGCACAGTCTGTGACCAAGCGGAGACGGCTGTGAGCGGATCGTGTG	2760
Db	2701	ATCTGGGCGATCGCACAGTCTGTGACCAAGCGGAGACGGCTGTGAGCGGATCGTGTG	2760
QY	2761	CTCGCCACCGCTAGCGCTCCGGATCGGTACCGGTCCACATCCAAACATCGAGAGGTG	2820

Db	2761	CTGCACCCGCTACGGCTCCGGGATCGGTACACCGGTGCCACATCCAAATCATCGAGGAAGTG	2820
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGSCAAAGCCATCCCATTCGAGACATC	2880
Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGSCAAAGCCATCCCATTCGAGACATC	2880
Qy	2881	AAGGGGGGAGGACCCATTTTCTCCATTCGAGAAAGATGATGAGACTGGCCGG	2940
Db	2881	AAGGGGGGAGGACCCATTTTCTCCATTCGAGAAAGATGATGAGACTGGCCGG	2940
Qy	2941	AAGCTGTCCGGCCTCGGACCTCAATTCGTAGCATATTAACCGGGGCTTGATGTATCCGTC	3000
Db	2941	AAGCTGTCCGGCCTCGGACCTCAATTCGTAGCATATTAACCGGGGCTTGATGTATCCGTC	3000
Qy	3001	ATACCACTACGCGAGACCTCATTTGTCGTAGACAGAGGAGCGCTCATGATAGCGGTTTACG	3060
Db	3001	ATACCACTACGCGAGACCTCATTTGTCGTAGACAGAGGAGCGCTCATGATAGCGGTTTACG	3060
Qy	3061	GGGCATTTCGACTAGTACGATCGACTGCATATGATGTGTACCCAGACAGTCGACTTACG	3120
Db	3061	GGGCATTTCGACTAGTACGATCGACTGCATATGATGTGTACCCAGACAGTCGACTTACG	3120
Qy	3121	CTGGACCCGACCTTCACCATTTGAGACGAGACCGCTGSCCAAGAGCGGCTGACGCTCG	3180
Db	3121	CTGGACCCGACCTTCACCATTTGAGACGAGACCGCTGSCCAAGAGCGGCTGACGCTCG	3180
Qy	3181	CAGCGGCGACGACGAGCTGGTAGGGGAGAGATGGCGATTTAAGGTTTGTGACTCCAGGA	3240
Db	3181	CAGCGGCGACGACGAGCTGGTAGGGGAGAGATGGCGATTTAAGGTTTGTGACTCCAGGA	3240
Qy	3241	GAACGGCCCTCGGGCATGTTCCATTCCTCGGTTCTGTGCGAATGCTATGACGGCGCTGT	3300
Db	3241	GAACGGCCCTCGGGCATGTTCCATTCCTCGGTTCTGTGCGAATGCTATGACGGCGCTGT	3300
Qy	3301	GCTTGTACGAGCTCACGCGCGCGAGACCTCATGTAAGTTTCGGGCTTACTTAACACA	3360
Db	3301	GCTTGTACGAGCTCACGCGCGCGAGACCTCATGTAAGTTTGGGGCTTACTTAACACA	3360
Qy	3361	CCAGGCTTGCCCGTCTGCGAAGAACCATCTGGAATTTGSGAGAGCGTCTTTACAGGCTC	3420
Db	3361	CCAGGCTTGCCCGTCTGCGAAGAACCATCTGGAATTTGSGAGAGCGTCTTTACAGGCTC	3420
Qy	3421	ACCACATAGACGCCCATTTCTTGTCCCAACACTAACGAGGAGAGAACACTCCCTAC	3480
Db	3421	ACCACATAGACGCCCATTTCTTGTCCCAACACTAACGAGGAGAGAACACTCCCTAC	3480
Qy	3481	CTGTGATGATACCAAGGCTACGGTGTGGCGCAGGAGGCTCCAGGCTCCACCTCATCGTGGAC	3540
Db	3481	CTGTGATGATACCAAGGCTACGGTGTGGCGCAGGAGGCTCCAGGCTCCACCTCATCGTGGAC	3540
Qy	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAACCTTACGCTGCACGGGCGCAAGCGCCCTGCTG	3600
Db	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAACCTTACGCTGCACGGGCGCAAGCGCCCTGCTG	3600
Qy	3601	TATAGCTGGGAGCGGTTCAAAAGAGAGTTACTACCACACACCCATAACCAATATATC	3660
Db	3601	TATAGCTGGGAGCGGTTCAAAAGAGAGTTACTACCACACACCCATAACCAATATATC	3660
Qy	3661	ATGGCATGATGCGGCTGACCTGAGAGTGTGTACAGGCAAGCTCGTGCTGTAGCGGA	3720
Db	3661	ATGGCATGATGCGGCTGACCTGAGAGTGTGTACAGGCAAGCTCGTGCTGTAGCGGA	3720
Qy	3721	GTCCTAGCAGCTCTGCGCGGTATTCGCTGACAAACAGCAGCGCTGCTATTTGSGGACAG	3780
Db	3721	GTCCTAGCAGCTCTGCGCGGTATTCGCTGACAAACAGCAGCGCTGCTATTTGSGGACAG	3780
Qy	3781	ATCATTTTCCGGAAGCGCGGCATATTTCCGACAGGGAAGTCTTTACCGGGAGTTT	3840
Db	3781	ATCATTTTCCGGAAGCGCGGCATATTTCCGACAGGGAAGTCTTTACCGGGAGTTT	3840
Qy	3841	GATGAGATGAGAGATGTGGGCTCACCTGCTTACATCGAAGAGGAATGACGCTCGC	3900
Db	3841	GATGAGATGAGAGATGTGGGCTCACCTGCTTACATCGAAGAGGAATGACGCTCGC	3900

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QY 3901 GAACATTTCAACAGAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGCT 3960
DB 3901 GAACATTTCAACAGAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGCT 3960
QY 3961 GCTGCTCCGGTGGTGGATCCAGTGGGGAGACCCCTCGAAGCTTCTGGGGCAACATATG 4020
DB 3961 GCTGCTCCGGTGGTGGATCCAGTGGGGAGACCCCTCGAAGCTTCTGGGGCAACATATG 4020
QY 4021 TGGAAATTCATCAGCGGGATACATATTTAGCAGGCTGTGCTGCTGCTGCAACCC 4080
DB 4021 TGGAAATTCATCAGCGGGATACATATTTAGCAGGCTGTGCTGCTGCTGCAACCC 4080
QY 4081 GCGATAGCATCATGTAGGCAATTCACAGCTCTATCACAGCCGCTCACCACCAACAT 4140
DB 4081 GCGATAGCATCATGTAGGCAATTCACAGCTCTATCACAGCCGCTCACCACCAACAT 4140
QY 4141 ACCCTCCTGTTTAACTCCTGGGGGATGGGTGGCCGCCCAACTTGCCTCCAGGCT 4200
DB 4141 ACCCTCCTGTTTAACTCCTGGGGGATGGGTGGCCGCCCAACTTGCCTCCAGGCT 4200
QY 4201 GCTTCTGCTTGTAGGCGCGCATCGCTGAGAGCGCTGTTGGCAGCATAGGCTTGGG 4260
DB 4201 GCTTCTGCTTGTAGGCGCGCATCGCTGAGAGCGCTGTTGGCAGCATAGGCTTGGG 4260
QY 4261 AAGTCTGTGATATTTTGGCAGATTATGAGCAGGGGTGGCAGGCGCGCTGCTGAGC 4320
DB 4261 AAGTCTGTGATATTTTGGCAGATTATGAGCAGGGGTGGCAGGCGCGCTGCTGAGC 4320
QY 4321 TTTTAAAGTATGAGCGGCGAGATGCCCTCCACGAGACCTGCTAACCTTCTCCTGCT 4380
DB 4321 TTTTAAAGTATGAGCGGCGAGATGCCCTCCACGAGACCTGCTAACCTTCTCCTGCT 4380
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DB 4381 ATCCTCCCGCTGGCGCTAGTCGTCGAGGCTGCTGTCGCGCAGCATACTGCTGCGGAC 4440
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DB 4441 GTGGGCCCAAGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCTTGCCTTGC 4500
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DB 4501 GGTAAACAGTCTCCCCCAGCAGCATGTGCTGAGAGGAGCGCTGACAGAGTGCAT 4560
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DB 4561 CAGATCTCTCTAGTCTTACCATCACTAGCTGCTGAAGAGGCTTACACAGTGCATAC 4620
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PN WO00238793-A2.
XX
PD 16-MAY-2002.
XX
PF 02-NOV-2001; 2001WO-US46350.
XX
PR 07-NOV-2000; 2000US-245866P.
XX
PA (ANAD-) ANADYS PHARM INC.
XX
PI Bichko V.
XX
DR WPI; 2002-49082/52.
XX
PT Novel nucleic acid encoding replication competent recombinant hepatitis
PT C virus genome useful for screening anti-hepatitis C virus therapeutics
PT and for vaccine development
XX
PS Claim 11; Page 70-75; 85pp; English.
XX
CC The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement
CC non-infectious, replication-defective infection-component, and
CC replication-defective non-infectious HCV, in gene therapy or gene
CC vaccination targeted to hepatic tissue for treating an animal infected or
CC susceptible to HCV infection and for studying HCV infection and
CC propagation. The present sequence is a clone of a fragment of the HCV
CC genome designated HCV824.
XX
SO Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 other;
Query Match 99.98; Score 7984; DB 24; Length 7992;
Best Local Similarity 99.98; Pired. No. 0;
Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 GCAGAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTGTAGAGAACTACTG 60
DB 1 GCAGAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTGTAGAGAACTACTG 60
OY 61 TCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCAAGCTCCAGAGC 120
DB 61 TCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCAAGCTCCAGAGC 120
OY 121 CCCCCCTCCGGGAGAGCGATAGTGTCTGGAGACCGGTGATACACGGAAATTCGAC 180
DB 121 CCCCCCTCCGGGAGAGCGATAGTGTCTGGAGACCGGTGATACACGGAAATTCGAC 180
OY 181 GACGACGGGTCTTCTTGGATACACCCGCTCAATCCCTGAGATTTGGGCGTGGCCCC 240
DB 181 GACGACGGGTCTTCTTGGATACACCCGCTCAATCCCTGAGATTTGGGCGTGGCCCC 240
OY 181 GACGACGGGTCTTCTTGGATACACCCGCTCAATCCCTGAGATTTGGGCGTGGCCCC 240
DB 181 GACGACGGGTCTTCTTGGATACACCCGCTCAATCCCTGAGATTTGGGCGTGGCCCC 240
OY 241 GCGAAGCTGACGCGAGTAGTGTGGGTGCGGAAAGCGCTTGGGACTGCTGATAG 300
DB 241 GCGAAGCTGACGCGAGTAGTGTGGGTGCGGAAAGCGCTTGGGACTGCTGATAG 300
OY 301 GTGCTTGGAGTGGCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGAAATCTTAAC 360
DB 301 GTGCTTGGAGTGGCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGAAATCTTAAC 360
OY 361 CTCAGAGAAAAACCAAGGGGGCGGCATGATTGAACAAGATGGATTGACAGCAGGTTCTC 420
DB 361 CTCAGAGAAAAACCAAGGGGGCGGCATGATTGAACAAGATGGATTGACAGCAGGTTCTC 420
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DB 421 CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACAGACAATCGCTGCT 480

OY 481 CTGATGCCGCGGTGTTCGGGCTGTACGCGCAGGGGCGCCGGTCTTTTGTACAGACCG 540
DB 481 CTGATGCCGCGGTGTTCGGGCTGTACGCGCAGGGGCGCCGGTCTTTTGTACAGACCG 540
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DB 541 ACCTGTCCGGTCCCTGAAATGAATGACAGAGCAGCGCGGCTATCGTGTGGCCA 600
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Db 5521 AGGGAAGTATCGTCTCGCGCGAGATCTGCGAGAGTCCAGGAATTCCTCTGAGCGATG 5580
Qy 5581 CCCATATGAGCAGCGCGGATTTCAACCTCCACTGTATAGATCTCTGGAAGGACCCGGAC 5640
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Db 5821 ACGGCTCTCTCTGACAGCCCTTCGAGAGCGGCGAGGATCCGAGCTTGTAGTCTGAC 5880
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Db 7981 AGATCAAGTACT 7992
| | | | |

RESULT 3
AAA98968
ID AAA98968 standard; DNA; 7989 BP.
XX
AC AAA98968:

XX 08-FEB-2001 (first entry)
XX Hepatitis C virus DNA fragment SEQ ID NO: 4.
XX Cell culture; therapy; infection; vaccine; diagnosis; gene therapy; ds.
XX Hepatitis C virus.
XX DE1915178-A1.
XX 05-OCT-2000.
XX 03-APR-1999; 99DE-1015178.
XX 03-APR-1999; 99DE-1015178.
XX (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX Bartenschlager R;
XX WPI; 2000-629140/61.
XX Cell culture system for hepatitis C virus, useful e.g. in screening for
XX therapeutic agents, comprises human hepatoma cells containing a viral
XX RNA construct that includes a selectable gene -
XX
XX Claim 8; Page 37-43; 58pp; German.
XX This invention describes a novel Hepatitis C virus (HCV) cell culture
XX system comprising human hepatoma cells that contain an integrated HCV-RNA
XX construct (I). (I) contains the HCV-specific RNA segments 5'-NTR
XX (non-translated region), NS (non-structural)3, NS4A, NS4B, NS5A, NS5B and
XX 3'-NTR, and a selectable (marker) gene (II). The cell cultures, and/or
XX (I), are used to prepare, evaluate and/or test therapeutic and/or
XX diagnostic agents for HCV infections, and to prepare vaccines against HCV
XX infection (particularly preparation of attenuated HCV). The can also be
XX used for preparation of a liver-specific delivery system for gene
XX therapy, and to identify cells permissive for HCV replication. Virus RNA
XX replicates autonomously and with high efficiency in this cellular system,
XX so that variations in replication rates can be measured (for screening
XX antiviral agents) quantitatively or qualitatively, using standard
XX laboratory equipment. Efficient replication of HCV RNA is only achieved
XX when the specified RNA segments are present and when the transfected
XX cells are maintained under permanent selection pressure.
XX
XX Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 other;
XX
XX Query Match 99.9%; Score 7982.6; DB 21; Length 7989;
XX Best Local Similarity 99.9%; Pred. No. 0; Mismatches 4; Indels 0; Gaps 0;
XX Matches 7985; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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XX 1 GCAGAGCCCGATGGGGGAGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60
XX 1 GCAGAGCCCGATGGGGGAGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60
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Db	1441	GTTCCTCTGGAAGCTTCTTGAAGCAAAACAAAGTCTGTAGGACCTTTGCGAGCAGCG	1500
Qy	1501	AACCCCCCACTGGGACAGGTGCTCTGCGGCCAAAGCCACGCTGTATGATACACT	1560
Db	1501	AACCCCCCACTGGGACAGGTGCTCTGCGGCCAAAGCCACGCTGTATGATACACT	1560
Qy	1561	GCAAAAGCGGCAACACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAA	1620
Db	1561	GCAAAAGCGGCAACACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAA	1620
Qy	1621	TGGCTCTCTCAAGCGTATTCAACAAGGGGCTGGAAGGATGCCCGAAGAGTACCCCATTTG	1680
Db	1621	TGGCTCTCTCAAGCGTATTCAACAAGGGGCTGGAAGGATGCCCGAAGAGTACCCCATTTG	1680
Qy	1681	ATGGATCTGATGTGGGCGCTCGTGACATCTTTAATGTTGTTAGTCCAGGTTAAA	1740
Db	1681	ATGGATCTGATGTGGGCGCTCGTGACATCTTTAATGTTGTTAGTCCAGGTTAAA	1740
Qy	1741	AACGCTTAGGCCCCCGAAACACGGGGAGCTGTTTCCTTTGAAAACACGATATATCC	1800
Db	1741	AACGCTTAGGCCCCCGAAACACGGGGAGCTGTTTCCTTTGAAAACACGATATATCC	1800
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Db	1861	AGCCTCACAGCGCGGACAGGAACACAGTGTGAGGGGAGGTCACAGTGTCTCACGCA	1920
Qy	1921	ACGCAATCTTCTCGGCGACCTCGTCATGAGGGGTGTGTGAGCTGTATCATATGATCC	1980
Db	1921	ACGCAATCTTCTCGGCGACCTCGTCATGAGGGGTGTGTGAGCTGTATCATATGATCC	1980
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Db	1981	GCGCTCAAGAACCCTTGCCGCGCCAAAGGGGCCAATACCACCAATGTACACCATGTGAC	2040
Qy	2041	CAGGACTCGTGGGCTGCGCAAGCGCCCCCGGGGGCGCTTCTTACACACATGACACGCG	2100
Db	2041	CAGGACTCGTGGGCTGCGCAAGCGCCCCCGGGGGCGCTTCTTACACACATGACACGCG	2100
Qy	2101	GCGAGCTCGACCTTACTGTGTCAAGAGGCAATGCCGATGTATTCGGGTGGCGGGCG	2160
Db	2101	GCGAGCTCGACCTTACTGTGTCAAGAGGCAATGCCGATGTATTCGGGTGGCGGGCG	2160
Qy	2161	GGCGACAGCAGGGGGAACCTACTCTCCCCAGGCCGTCTCTACTTGAAGGGCTCTTCG	2220
Db	2161	GGCGACAGCAGGGGGAACCTACTCTCCCCAGGCCGTCTCTACTTGAAGGGCTCTTCG	2220
Qy	2221	GGGCGTCACTGCGTACCCCTCGGGGACAGCTGTGGGATCTTTGGGCTCCCTGTGCG	2280
Db	2221	GGGCGTCACTGCGTACCCCTCGGGGACAGCTGTGGGATCTTTGGGCTCCCTGTGCG	2280
Qy	2281	ACCCGAGGGGTGGAGAGCGGTGACATTTGATACCCGTCAGATCTATGGAACACACTATG	2340
Db	2281	ACCCGAGGGGTGGAGAGCGGTGACATTTGATACCCGTCAGATCTATGGAACACACTATG	2340
Qy	2341	CGGTCGCCGGTCTTACAGGCAACATGTGTCGCCGCGGTACCGGACATTTCCAGGTG	2400
Db	2341	CGGTCGCCGGTCTTACAGGCAACATGTGTCGCCGCGGTACCGGACATTTCCAGGTG	2400
Qy	2401	GCCCATCTACACGCCCTTACTGTGATGAGGACACTAAGGTGCCGCTGCTATGCA	2460
Db	2401	GCCCATCTACACGCCCTTACTGTGATGAGGACACTAAGGTGCCGCTGCTATGCA	2460
Qy	2461	GCCCAAGGATTAAGGTGCTTGTCTGTAACCGTCCGTGGCGCACCTTAAGTTTCGG	2520
Db	2461	GCCCAAGGATTAAGGTGCTTGTCTGTAACCGTCCGTGGCGCACCTTAAGTTTCGG	2520

QY	2521	GGGTAATGTCTAAGGCACATAGTATGTGACCCCTTAACATCAGAAACGGGGGTAAAGACATC	2580
Db	2521	GGGTAATGTCTAAGGCACATAGTATGTGACCCCTTAACATCAGAAACGGGGGTAAAGACATC	2580
QY	2581	ACGACGGGTGCCCCCTACACGACTCCACCACTATGGCAAGTTTCTTGCCGACGGTGGTTGC	2640
Db	2581	ACGACGGGTGCCCCCTACACGACTCCACCACTATGGCAAGTTTCTTGCCGACGGTGGTTGC	2640
QY	2641	TCGTGGGCGCCCTATGACATCTAATAATATGTATATAGTCCACCTCACTCACTGACCAACT	2700
Db	2641	TCGTGGGCGCCCTATGACATCTAATAATATGTATATAGTCCACCTCACTCACTGACCAACT	2700
QY	2701	ATCTGGGACATCGGCGACATCTCTGGACCACGAGAGCGGCTGGAGCGGACTCGTCGTG	2760
Db	2701	ATCTGGGACATCGGCGACATCTCTGGACCACGAGAGCGGCTGGAGCGGACTCGTCGTG	2760
QY	2761	CTGCGCCACCGCCTACGCTCCGGGATCGGGTCAACGCTGCACATCCAAACATCGAGGAGGTG	2820
Db	2761	CTGCGCCACCGCCTACGCTCCGGGATCGGGTCAACGCTGCACATCCAAACATCGAGGAGGTG	2820
QY	2821	GCTCTGTCCAGCACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACATC	2880
Db	2821	GCTCTGTCCAGCACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACATC	2880
QY	2881	AAGGGGGGAGGAGCACTCATTTTTCGSCATTCCAAAGAAATGTGATAGCTCGGCGG	2940
Db	2881	AAGGGGGGAGGAGCACTCATTTTTCGSCATTCCAAAGAAATGTGATAGCTCGGCGG	2940
QY	2941	AAGCTGTCCGGCCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGAATGATCCGC	3000
Db	2941	AAGCTGTCCGGCCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGAATGATCCGC	3000
QY	3001	ATACCACTAGGGGAGACGTCATGTGCGAGCAAGCGGCGCTGAATGACGGGCTTTTAC	3060
Db	3001	ATACCACTAGGGGAGACGTCATGTGCGAGCAAGCGGCGCTGAATGACGGGCTTTTAC	3060
QY	3061	GGCGATTTCGACTAGTGAATGCACTGTGCATATGTGTCAACCAGACATCGACTTCACG	3120
Db	3061	GGCGATTTCGACTAGTGAATGCACTGTGCATATGTGTCAACCAGACATCGACTTCACG	3120
QY	3121	CTGGACCCGACCTTCACCATTTGAGAGAGACCGCTGTGTCACGAGACGCTCTAATGACGGGCTTTAC	3180
Db	3121	CTGGACCCGACCTTCACCATTTGAGAGAGACCGCTGTGTCACGAGACGCTCTAATGACGGGCTTTAC	3180
QY	3181	CAGCGGCGAGGACAGGACTGTAAGGGGACAGATGGGCAATTACAGTTTGTGACTCCAGCA	3240
Db	3181	CAGCGGCGAGGACAGGACTGTAAGGGGACAGATGGGCAATTACAGTTTGTGACTCCAGCA	3240
QY	3241	GAAAGGCGCTCGGGGCAATGTTGATTCATTCCTCGGTTCTGTGCGAGTCTATGACGGGGCTGT	3300
Db	3241	GAAAGGCGCTCGGGGCAATGTTGATTCATTCCTCGGTTCTGTGCGAGTCTATGACGGGGCTGT	3300
QY	3301	GCTTGTGTAAGGACTCACGCGCCGCGAGACCTCAGTTAGGTTCGGGCTTACTTAAACACA	3360
Db	3301	GCTTGTGTAAGGACTCACGCGCCGCGAGACCTCAGTTAGGTTCGGGCTTACTTAAACACA	3360
QY	3361	CGAGGTTGCGCCGCTGCGCCAGGACATCTGGAGTTCTGGAGAGACGCTTTACAGGCGCTC	3420
Db	3361	CGAGGTTGCGCCGCTGCGCCAGGACATCTGGAGTTCTGGAGAGACGCTTTACAGGCGCTC	3420
QY	3421	ACCCACATAGACGCCCATTTTCTTGTCCAGACTAAGCAGGCGAGGACATCTCCCTAC	3480
Db	3421	ACCCACATAGACGCCCATTTTCTTGTCCAGACTAAGCAGGCGAGGACATCTCCCTAC	3480
QY	3481	CTGGAGATATCCAGGCTACGGTGTGTCGGCAGAGGCTCGAGGCTCCACCTCATCTGTGGAC	3540
Db	3481	CTGGAGATATCCAGGCTACGGTGTGTCGGCAGAGGCTCGAGGCTCCACCTCATCTGTGGAC	3540
QY	3541	CAAAATGTGAAGTGTCTCATAGGCTTAAAGCTTACGCTGCACGGGCGCAAGCGCCCTGTG	3600
Db	3541	CAAAATGTGAAGTGTCTCATAGGCTTAAAGCTTACGCTGCACGGGCGCAAGCGCCCTGTG	3600

QY 3601 TATAGCTGGAGCGCTTCACAAACGAGTTACTACACACCCCAATACCAATACATC 3660
DB 3601 TATAGCTGGAGCGCGCTTCAAAACGAGTTACTACACACCCCAATACCAATACATC 3660
QY 3661 ATGCATCATGTGGGCTGACCTGAGGTGCTACAGACACCTGGGTCTGGTAGCGGA 3720
DB 3661 ATGCATCATGTGGGCTGACCTGAGGTGCTACAGACACCTGGGTCTGGTAGCGGA 3720
QY 3721 GTCACAGAGCTGTGGCGCGTATTGCTGACACAGACAGCGTGTGAGGAGG 3780
DB 3721 GTCACAGAGCTGTGGCGCGTATTGCTGACACAGACAGCGTGTGAGGAGG 3780
QY 3781 ATCATCTTGTCCGGAAGCGCCCATCATCTCCGACAGGAGTCTTTACCGGAGTTC 3840
DB 3781 ATCATCTTGTCCGGAAGCGCCCATCATCTCCGACAGGAGTCTTTACCGGAGTTC 3840
QY 3841 GATGAGATGAGAGTGGGCGCTCACACCTCCCTTACATCGAACAGGAGATGCACTGCC 3900
DB 3841 GATGAGATGAGAGTGGGCGCTCACACCTCCCTTACATCGAACAGGAGATGCACTGCC 3900
QY 3901 GACCAATTCACACAGAGGCAATCGGCTGCTGCAACACAGCCACCAAGCAGCGAGCT 3960
DB 3901 GACCAATTCACACAGAGGCAATCGGCTGCTGCAACACAGCCACCAAGCAGCGAGCT 3960
QY 3961 GCTGCTCCCGTGTGGATCCAGTGGGCGACCTCCAGAGCTTCTGGGGAGGCAATAG 4020
DB 3961 GCTGCTCCCGTGTGGATCCAGTGGGCGACCTCCAGAGCTTCTGGGGAGGCAATAG 4020
QY 4021 TGGAAATTCATCAGCGGATACAAATATTAGACGCTGTCTCACTCTGCTCCAGACCC 4080
DB 4021 TGGAAATTCATCAGCGGATACAAATATTAGACGCTGTCTCACTCTGCTCCAGACCC 4080
QY 4081 GCGATAGCATCTAGTGGCATTCACAGCTCTATCACACCCCGGCTCACACCAAT 4140
DB 4081 GCGATAGCATCTAGTGGCATTCACAGCTCTATCACACCCCGGCTCACACCAAT 4140
QY 4141 ACCCTCTGTTTAACTCCTGGGGGAGTGGGCGCCCACTTGTCTCTCCAGCGCT 4200
DB 4141 ACCCTCTGTTTAACTCCTGGGGGAGTGGGCGCCCACTTGTCTCTCCAGCGCT 4200
QY 4201 GCTTCTGCTTGTAGGCGCGGCAATCGCTGAGAGGCTGTGGCAGATAGGCGCTTGG 4260
DB 4201 GCTTCTGCTTGTAGGCGCGGCAATCGCTGAGAGGCTGTGGCAGATAGGCGCTTGG 4260
QY 4261 AAGGCTGTGATATTTTGGCAGTTATGAGCAGGAGGTGGAGAGCGGCTCTGTGGC 4320
DB 4261 AAGGCTGTGATATTTTGGCAGTTATGAGCAGGAGGTGGAGAGCGGCTCTGTGGC 4320
QY 4321 TTTAAGTCATGAGCGGCGAGATGCCCTTCACCGAGACCTGCTTACTCTCCCTGCT 4380
DB 4321 TTTAAGTCATGAGCGGCGAGATGCCCTTCACCGAGACCTGCTTACTCTCCCTGCT 4380
QY 4381 ATCTCTCCCTGGGCGCTTGTGCGGGGCTGTGCGAGCAGATCTGCTTACTCTCCCTGCT 4440
DB 4381 ATCTCTCCCTGGGCGCTTGTGCGGGGCTGTGCGAGCAGATCTGCTTACTCTCCCTGCT 4440
QY 4441 GTGGGCCCAAGGAGGAGGCTGTGCAATGATGAACCGGCTGATAGCTTGGCTTGGG 4500
DB 4441 GTGGGCCCAAGGAGGAGGCTGTGCAATGATGAACCGGCTGATAGCTTGGCTTGGG 4500
QY 4501 GGTAAACAGGTCCTCCCGCAGCAGATGTGCTGAGAGGAGCGGCGAGCAGCTGCTACT 4560
DB 4501 GGTAAACAGGTCCTCCCGCAGCAGATGTGCTGAGAGGAGCGGCGAGCAGCTGCTACT 4560
QY 4561 CAGATCTCTCTAGTCTTACATCACTAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC 4620
DB 4561 CAGATCTCTCTAGTCTTACATCACTAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC 4620
QY 4621 GAGGACTGCTCCAGCGCATGCTCCGGCTGAGGCTAAGAGATGTTGGATTGGATTAGC 4680
DB 4621 GAGGACTGCTCCAGCGCATGCTCCGGCTGAGGCTAAGAGATGTTGGATTGGATTAGC 4680
QY 4681 ACGGTGTGACTGATTTCAAGACCTGGCTCAAGTCCAACTCTCTCCGCGATTCGCGGGA 4740

DB 4681 ACGGTGTGACTGATTTCAAGACCTGGCTCAGTCCAAAGCTCTCTCCGCGATTCGCGGGA 4740
QY 4741 GTCCCTCTCTCTATGTCACAGGAGTGTGAGGAGTGTGGGGGCGAGGCGATCATG 4800
DB 4741 GTCCCTCTCTCTATGTCACAGGAGTGTGAGGAGTGTGGGGGCGAGGCGATCATG 4800
QY 4801 CAAACACCTGCGCATGTGAGCAGATCACCAGGACATGTGAAGGAGTTCATGAGG 4860
DB 4801 CAAACACCTGCGCATGTGAGCAGATCACCAGGACATGTGAAGGAGTTCATGAGG 4860
QY 4861 ATCGTGGGCGCTTAGAGCTGTAGTACACGAGGATGAACATTTCCCATTAACGCTAG 4920
DB 4861 ATCGTGGGCGCTTAGAGCTGTAGTACACGAGTGAACATTTCCCATTAACGCTAG 4920
QY 4921 ACCAGGCGCGCTGACGCGCTCCCGCGGCGCAATTTATTCTAGGCGCTGTGGCGGTG 4980
DB 4921 ACCAGGCGCGCTGACGCGCTCCCGCGGCGCAATTTATTCTAGGCGCTGTGGCGGTG 4980
QY 4981 GCTGCTGAGAGTACGTGAGAGTACGCGGCTGGGGGATTTCCACTACGTAGAGGCGATG 5040
DB 4981 GCTGCTGAGAGTACGTGAGAGTACGCGGCTGGGGGATTTCCACTACGTAGAGGCGATG 5040
QY 4981 GCTGCTGAGAGTACGTGAGAGTACGCGGCTGGGGGATTTCCACTACGTAGAGGCGATG 5040
DB 4981 GCTGCTGAGAGTACGTGAGAGTACGCGGCTGGGGGATTTCCACTACGTAGAGGCGATG 5040
QY 5041 ACCACTGACACGTTAAAGTCCCGTGTGACAGTTCCGCGCCCGCAATTTCTTACAGAGT 5100
DB 5041 ACCACTGACACGTTAAAGTCCCGTGTGACAGTTCCGCGCCCGCAATTTCTTACAGAGT 5100
QY 5101 GATGGGCTGCGGTTGCAAGATGAGCTTCACAGGCTTCACAGGCTTCCAGGAGAGGCT 5160
DB 5101 GATGGGCTGCGGTTGCAAGATGAGCTTCACAGGCTTCACAGGCTTCCAGGAGAGGCT 5160
QY 5161 ACATTCCTGTCGCGGCTCAATCAATACCTGTTGGGTGACAGCTCCCATCGAGCCGAA 5220
DB 5161 ACATTCCTGTCGCGGCTCAATCAATACCTGTTGGGTGACAGCTCCCATCGAGCCGAA 5220
QY 5221 CCGGAGTACAGTGTCTCACTTCCATGCTTCACAGGCTTCCAGGCTTCCAGGAGAGG 5280
DB 5221 CCGGAGTACAGTGTCTCACTTCCATGCTTCACAGGCTTCCAGGCTTCCAGGAGAGG 5280
QY 5281 GCTAAGCGTAGGCTGGCGAGGAGTCTCCCGCTCTTGGGCGAGCTCATGAGTACGAG 5340
DB 5281 GCTAAGCGTAGGCTGGCGAGGAGTCTCCCGCTCTTGGGCGAGCTCATGAGTACGAG 5340
QY 5341 CTGTCTGCGGCTTCTTGAAGCAATGACATACCGTCACTGACTCCCGGAGCGTAC 5400
DB 5341 CTGTCTGCGGCTTCTTGAAGCAATGACATACCGTCACTGACTCCCGGAGCGTAC 5400
QY 5401 CTCATGAGAGGCAACCTCTGTGGCGGAGAGATGGGCGGAACTACACCGGCTGAG 5460
DB 5401 CTCATGAGAGGCAACCTCTGTGGCGGAGAGATGGGCGGAACTACACCGGCTGAG 5460
QY 5461 TCAGAAATTAAGTATGATTTTGGAGCTTTGAGCGCTTCAGCGCTTCAGCGGAGAGATGAG 5520
DB 5461 TCAGAAATTAAGTATGATTTTGGAGCTTTGAGCGCTTCAGCGGCTTCAGCGGAGAGATGAG 5520
QY 5521 AAGGAGTATTCGTTCCCGGCGAGATCTGCGGAGAGTCCAGGAATTTCCCTGAGCATG 5580
DB 5521 AAGGAGTATTCGTTCCCGGCGAGATCTGCGGAGAGTCCAGGAATTTCCCTGAGCATG 5580
QY 5581 CCCATATGAGGCGCGCGGATTCACACCTCCACTGTTAGAGTCTGTGAAGAGACCGGAG 5640
DB 5581 CCCATATGAGGCGCGCGGATTCACACCTCCACTGTTAGAGTCTGTGAAGAGACCGGAG 5640
QY 5641 TACGTCCTCTCAGTGTACAGGAGTGTGCAATTTGCGGCTTGCAGAGCGGCTTCGATACCA 5700
DB 5641 TACGTCCTCTCAGTGTACAGGAGTGTGCAATTTGCGGCTTGCAGAGCGGCTTCGATACCA 5700
QY 5701 CTTCCAGGAGAGAGAGAGAGGCTTCTCTGTCAGATCTAACGCTTCTTCTGCTTGGCG 5760
DB 5701 CTTCCAGGAGAGAGAGAGAGGCTTCTCTGTCAGATCTAACGCTTCTTCTGCTTGGCG 5760
QY 5761 GAGCTGCGCAAAAGACTTGGGAGCTCCGAGTCCGAATGCTGGCGCTGACAGGCGGAGCA 5820

Db	5761	GAGCTGCCCAAAAGACCTTCGGCAGCTCCGAAATGTCGGCCCTGCACAGCGGAGCGCA	5820
Qy	5821	ACGGCCTCTCCTTACCGAGCCCTTCGCAGCAGCGGCAGCGCGGATATCCAGCTTGAAGTGTAC	5880
Db	5821	ACGGCCTCTCCTTACCGAGCCCTTCGCAGCAGCGGCAGCGCGGATATCCAGCTTGAAGTGTAC	5880
Qy	5881	TCCTCCAAAGCCCCCCTTGAAGGGGAGCGCGGGGGATCCCGATCTCAGAGAGGGTCTTGG	5940
Db	5881	TCCTCCAAAGCCCCCCTTGAAGGGGAGCGCGGGGGATCCCGATCTCAGAGAGGGTCTTGG	5940
Qy	5941	TCCTACCTTAAGCGAGAGAGCTAGTAGAGACGTGCTGCTGCTGATGTCTCTACACATGG	6000
Db	5941	TCCTACCTTAAGCGAGAGAGCTAGTAGAGACGTGCTGCTGCTGATGTCTCTACACATGG	6000
Qy	6001	ACAGAGCCCTTGATCACGCCATATGCGCTGGGGAGAGAAACCAAGCTGCCATCAATAGCATGG	6060
Db	6001	ACAGAGCCCTTGATCACGCCATATGCGCTGGGGAGAGAAACCAAGCTGCCATCAATAGCATGG	6060
Qy	6061	AGCAACTCTTTGGCTCCGCTACACCAACTTGGTATAGCTACACATCTCGACGCGCAGC	6120
Db	6061	AGCAACTCTTTGGCTCCGCTACACCAACTTGGTATAGCTACACATCTCGACGCGCAGC	6120
Qy	6121	CTCGCGGAGAGAAAGTCACTTTGACACAGCTGCAGGTCTTGGAGACCACTACCGGGAC	6180
Db	6121	CTCGCGGAGAGAAAGTCACTTTGACACAGCTGCAGGTCTTGGAGACCACTACCGGGAC	6180
Qy	6181	GTGGCTCAAGGAGATGAAGGGGAGGGGCTCACAGTTAAGGGCTCAATCTCTATCCGTGGAG	6240
Db	6181	GTGGCTCAAGGAGATGAAGGGGAGGGGCTCACAGTTAAGGGCTCAATCTCTATCCGTGGAG	6240
Qy	6241	GAAGCCTGTAAAGCTGAGCGCCGCCACATTTGGGCCAGATCTAAATTTGCTATGGGGCAAG	6300
Db	6241	GAAGCCTGTAAAGCTGAGCGCCGCCACATTTGGGCCAGATCTAAATTTGCTATGGGGCAAG	6300
Qy	6301	GACGTCCGGAACTTATCCACAGAGGCGCGTTAAACCAATCCTGCTCGGTGGAGAGACTTG	6360
Db	6301	GACGTCCGGAACTTATCCACAGAGGCGCGTTAAACCAATCCTGCTCGGTGGAGAGACTTG	6360
Qy	6361	CTGGAAGACACTGAGACCAACCAATTTGACACCAACCATCATGGCAAAAATAGAGTTTTCGC	6420
Db	6361	CTGGAAGACACTGAGACCAACCAATTTGACACCAACCATCATGGCAAAAATAGAGTTTTCGC	6420
Qy	6421	GTTCACACCAAGAGAGGGGGCGCCAGACCAAGCTCGCCTTATGTATTCACAGATTTGGG	6480
Db	6421	GTTCACACCAAGAGAGGGGGCGCCAGACCAAGCTCGCCTTATGTATTCACAGATTTGGG	6480
Qy	6481	GTTCTGTGTGGAGAAATATGGCCCTTACAGATGTGTCTTCACCTCCCTAGAGCCCTG	6540
Db	6481	GTTCTGTGTGGAGAAATATGGCCCTTACAGATGTGTCTTCACCTCCCTAGAGCCCTG	6540
Qy	6541	ATGGGCTCTTCATAGGATTCCAATCTCTTCCTGACACAGCGGTGAGATTCCTGGTGAAT	6600
Db	6541	ATGGGCTCTTCATAGGATTCCAATCTCTTCCTGACACAGCGGTGAGATTCCTGGTGAAT	6600
Qy	6601	GCTCGAAAGCAACAAATGCGCATGCGGCTTGCGATATGACACCGCGCTTTTATACCA	6660
Db	6601	GCTCGAAAGCAACAAATGCGCATGCGGCTTGCGATATGACACCGCGCTTTTATACCA	6660
Qy	6661	ACGGTCACTGAGAAATGACATCCGTGTTAGAGAGTCAATCTACCAATGTTGATCTTGGCC	6720
Db	6661	ACGGTCACTGAGAAATGACATCCGTGTTAGAGAGTCAATCTACCAATGTTGATCTTGGCC	6720
Qy	6721	CCCGAAGCCAGACAGGCCATATAGGTTCCTCACHAGAGGGCTTTACATCGGGGGCCCTTG	6780
Db	6721	CCCGAAGCCAGACAGGCCATATAGGTTCCTCACHAGAGGGCTTTACATCGGGGGCCCTTG	6780
Qy	6781	ACTAATTTCAAAGGGCAGAACTGCGGTATGCGCGGTGCCGCGAGCGGTGTACTGACG	6840
Db	6781	ACTAATTTCAAAGGGCAGAACTGCGGTATGCGCGGTGCCGCGAGCGGTGTACTGACG	6840
Qy	6841	ACCAGCTGCGGTAAATACCTTACATGTTACTTGAAGGCCCTTCGGCGCTGTGAGACTGCG	6900
Db	6841	ACCAGCTGCGGTAAATACCTTACATGTTACTTGAAGGCCCTTCGGCGCTGTGAGACTGCG	6900

QY	6901	AAGTCTCAGAGACTGACAGATGCTCGTATATCGGAGACGACCTTGTCGTATCTGTGGAAAGC	6960
Db	6901	AAGCTTCAGAGACTGACAGAGTCTGTATCGGAGACGACCTTGTCGTATCTGTGGAAAGC	6960
QY	6961	GGGGGAGCCCAAGAGGACGAGGGGAGACCTACGAGGCTTCACGAGAGGCTATGACTAGATAC	7020
Db	6961	GGGGGAGCCCAAGAGGACGAGGGGAGACCTACGAGGCTTCACGAGAGGCTATGACTAGATAC	7020
QY	7021	TCTGCCCCCTTGGGGACCCGCCAAACCAAGATACGACTTGGAGTTGATTAACATCATATGC	7080
Db	7021	TCTGCCCCCTTGGGGACCCGCCAAACCAAGATACGACTTGGAGTTGATTAACATCATATGC	7080
QY	7081	TCTTCACATGTTGATGTCGCGACGACGATGATGTGGCAAAAGGGGTGTACTATCTCACCGGT	7140
Db	7081	TCTTCACATGTTGATGTCGCGACGACGATGATGTGGCAAAAGGGGTGTACTATCTCACCGGT	7140
QY	7141	GACCCACACACCCCCCTTGCGGGGGCTGCGTGGGAGACAGTACGACACACTCCAGTCAAT	7200
Db	7141	GACCCACACACCCCCCTTGCGGGGGCTGCGTGGGAGACAGTACGACACACTCCAGTCAAT	7200
QY	7201	TCTGAGCTAGGCAACATCATCATGATATGGCCACCCTTGTGGGCAAGGATGATCCTGATG	7260
Db	7201	TCTGAGCTAGGCAACATCATCATGATATGGCCACCCTTGTGGGCAAGGATGATCCTGATG	7260
QY	7261	ACTATTTTCTTCATATCCTTTTAACTCAGAGAACAACTTGAAAGGCCCTGATTTGTACG	7320
Db	7261	ACTATTTTCTTCATATCCTTTTAACTCAGAGAACAACTTGAAAGGCCCTGATTTGTACG	7320
QY	7321	ATCTACGGGGGCTTACTACTCATTTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC	7380
Db	7321	ATCTACGGGGGCTTACTACTCATTTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC	7380
QY	7381	CATGGCCTTACCGCATTTTAACTCCAGTACTACTCCAGGAGAGTCAATAAGGGTGCCT	7440
Db	7381	CATGGCCTTACCGCATTTTAACTCCAGTACTACTCCAGGAGAGTCAATAAGGGTGCCT	7440
QY	7441	TCATCCTCAGGAACTTGTGGGATACCGCCCTTGCGAGTCTGGAGACATCGGGCCGAGAGT	7500
Db	7441	TCATCCTCAGGAACTTGTGGGATACCGCCCTTGCGAGTCTGGAGACATCGGGCCGAGAGT	7500
QY	7501	GTCCGCGCTAGGCTACTGTCACGAGGGGGAGGAGGCTAGCCACTGTGGCAAGTACCTCTC	7560
Db	7501	GTCCGCGCTAGGCTACTGTCACGAGGGGGAGGAGGCTAGCCACTGTGGCAAGTACCTCTC	7560
QY	7561	AACTGGGCACTAAGACCAAGCTCAAACTACTTCATTCGCCGCTGCTGCCAGTTGGAT	7620
Db	7561	AACTGGGCACTAAGACCAAGCTCAAACTACTTCATTCGCCGCTGCTGCCAGTTGGAT	7620
QY	7621	TATATCAGATGTTGGTGTGCTGTAAAGGGGGAGACATATATACAGCCTGTCTGCT	7680
Db	7621	TATATCAGATGTTGGTGTGCTGTAAAGGGGGAGACATATATACAGCCTGTCTGCT	7680
QY	7681	GGCCGACCCCGCTGTTCAATGTGTGCTACTCTCTACTTTCTTAAAGGTTAAGGATCATAT	7740
Db	7681	GGCCGACCCCGCTGTTCAATGTGTGCTACTCTCTACTTTCTTAAAGGTTAAGGATCATAT	7740
QY	7741	CTACACCCCAACCATGAGGAGGAGCTAAACACTCCAGGCAATAGGCACTCTGATTTT	7800
Db	7741	CTACACCCCAACCATGAGGAGGAGCTAAACACTCCAGGCAATAGGCACTCTGATTTT	7800
QY	7801	TTTTCCCTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTCTTT	7860
Db	7801	TTTTCCCTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTCTTT	7860
QY	7861	TTTTTCCTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	7861	TTTTTCCTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
QY	7921	TACGCTGTAAGAGTCCGAGAGCCGCTTGACGACGAGAGAGTGCAGATACAGGCTCTCTGC	7980
Db	7921	TACGCTGTAAGAGTCCGAGAGCCGCTTGACGACGAGAGAGTGCAGATACAGGCTCTCTGC	7980

QY	7981	AGATCAAGT	7989
Db	7981	AGATCAAGT	7989

RESULT 4
AAD25322
ID AAD25322 standard; cDNA; 7989 BP

AC	AAD25322;
XX	
DT	12-MAR-2002 (first entry)
XX	

Hepatitis C virus (HCV) replBartman/Availi CDNA.

KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 KW gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver
 KW ss.

OS Hepatitis C virus

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
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95	95	95
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100	100	100

PN WO200189364-A2.

PD 29-NOV-2001.

PF 23-MAY-2001; 2001WO-US16822

PR 23-MAY-2000; 2000US-0576989

PA (UNIW) UNIV WASHINGTON.

Rice CM, Blight KJ;

DR WPI; 2002-066755/09.

DR P-PSDB; AAEL5717.

PT Hepatitis C virus variants having greater transfection efficiency and ability to survive subpassage, useful as a vaccine for immunizing primate to the virus, comprise non-naturally occurring viral sequences

PS Claim 44; Page 69-71; 174pp; English.

The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive subpassage greater than HCV that have wild-type polypeptide coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for the generation of defined HCV virus stocks to develop *in vitro* and *in vivo* assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficient replication in cell culture, production of HCV variants with altered tissue or species tropism, establishment of alternative animal models for inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated HCV derivatives as possible vaccine candidates, engineering of attenuated or defective HCV derivatives for expression of

heterologous gene products for gene therapy and vaccine applications for utilisation of the HCV glycoproteins for targeted delivery of therapeutic agents to the liver or other cell types with appropriate receptors. Vaccine comprising these sequences is useful for inducing immunoprotection to HCV in a primate. The present sequence is Hepatitis C virus (HCV) replicon/antigen cDNA.

SQ Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 other;

Query Match	99.9%	Score 7981;	DB 24,	Length 7989;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 7984; Conservative	0;	Mismatches 5;	IndeIs 0;	Gaps 0;

QY	1	GAGAGCCCCGAAATGGGGGGCCACACCTCCACCATAGATCACTCCCGTGGAGAACTACTG	60
Db	1	GCCAGCCCCGATGGGGGGGACACTCCACCATAGATCACTCCCGTGGAGAACTACTG	60
QY	61	TCTTCAAGCAGAAAGCGTCTAGCCATGGCGTTAGTATAGTGTGTGCAACCTCCAGAC	120
Db	61	TCTTCAAGCAGAAAGCGTCTAGCCATGGCGTTAGTATAGTGTGTGCAACCTCCAGAC	120
QY	121	CCCCCCTCCCGGAGAGCCATAGTGTGTGGGACCGGGGATTAACCGGAAATGGCCAG	180
Db	121	CCCCCCTCCCGGAGAGCCATAGTGTGTGGGACCGGGGATTAACCGGAAATGGCCAG	180
QY	181	GAGACCGGGTCTCTTCTTGGATCAACCGCTCAATGCTGAGATTTGGCGTGGCCCC	240
Db	181	GAGACCGGGTCTCTTCTTGGATCAACCGCTCAATGCTGAGATTTGGCGTGGCCCC	240
QY	241	GCGAGACGTCTAGCCAGTAGTGTGGGTGCGCAAGAGCCCTTGTGTACTGTGCTATAG	300
Db	241	GCGAGACGTCTAGCCAGTAGTGTGGGTGCGCAAGAGCCCTTGTGTACTGTGCTATAG	300
QY	301	GTCGTTGCGAGTGTCCCGGGAGCGTCTGTAGACCGTGTACCATGAGCACGAATCTTAAC	360
Db	301	GTCGTTGCGAGTGTCCCGGGAGCGTCTGTAGACCGTGTACCATGAGCACGAATCTTAAC	360
QY	361	CTCAAGAAACCAAAAGGGCGCCGACATGATTGACAAATGATGTGCACGAGGTTCTC	420
Db	361	CTCAAGAAACCAAAAGGGCGCCGACATGATTGACAAATGATGTGCACGAGGTTCTC	420
QY	421	CGGCGCGTTGGGTGGAGAGGCTATTCGGCTATGACTGTGGACACACAGACATCGGCTGCT	480
Db	421	CGGCGCGTTGGGTGGAGAGGCTATTCGGCTATGACTGTGGACACAGACATCGGCTGCT	480
QY	481	CTGATGCGCGCGGTGTCCCGGCTGTACGGGCGAGGGGCGCCCGGTTCTTTTGTCAAGACG	540
Db	481	CTGATGCGCGCGGTGTCCCGGCTGTACGGGCGAGGGGCGCCCGGTTCTTTTGTCAAGACG	540
QY	541	ACCTGTCCGCTGCCCTGAATGATACGTGCAGACAGACAGGCGGGGCTATGTGTGGTGGCA	600
Db	541	ACCTGTCCGCTGCCCTGAATGATACGTGCAGACAGACAGGCGGGGCTATGTGTGGTGGCA	600
QY	601	GCAAGGGCGGTTCTCTTGCGAGTGTGTGCGACGTGTGTCACTGAAGCGGGAAAGGACTGGC	660
Db	601	GCAAGGGCGGTTCTCTTGCGAGTGTGTGCGACGTGTGTCACTGAAGCGGGAAAGGACTGGC	660
QY	661	TGCTATTGGCGGAAGTCCCGGGGCGAGATCTCCGTCACTCACTGCTCTCGCGAGA	720
Db	661	TGCTATTGGCGGAAGTCCCGGGGCGAGATCTCCGTCACTCACTGCTCTCGCGAGA	720
QY	721	AAATATCCATCATGTGCTGTAATGCGCGGGCTGCTACAGCTTGAATCCGGCTACTGTCC	780
Db	721	AAATATCCATCATGTGCTGTAATGCGCGGGCTGCTACAGCTTGAATCCGGCTACTGTCC	780
QY	781	CATTGCAGCACCAAGGAAACATGCGATCGAGGAGAGAGTACTGTGGATGGAGACGGTTC	840
Db	781	CATTGCAGCACCAAGGAAACATGCGATCGAGGAGAGAGTACTGTGGATGGAGACGGTTC	840
QY	841	TTGTGATCGAGTAGTCTGGACGAAGAGCATCGAGGGGCTCGGCGCAGCCGAATCTTTCG	900
Db	841	TTGTGATCGAGTAGTCTGGACGAAGAGCATCGAGGGGCTCGGCGCAGCCGAATCTTTCG	900

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OY 901 CCAGGCTCAAGGCGCGCATGCCGACGCGAGGATCTCGTCTGAGCCATGGGAGTCCT 960
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Db 901 CCAGGCTCAAGGCGCGCATGCCGACGCGAGGATCTCGTCTGAGCCATGGGAGTCCT 960
OY 961 GCTTGCGGAATATCATGCTGGAATAATGGCCGCTTTTCTGTGATTCATGCACTGTGGCCGCG 1020
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OY 1021 TGGGATGAGGCGACGCTATCAGACATAGCTTGGGTACCCGTGATATTGCTGAGAGAC 1080
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Db 1021 TGGGATGAGGCGACGCTATCAGACATAGCTTGGGTACCCGTGATATTGCTGAGAGAC 1080
OY 1081 TTGGGCGGGAATGGGCTGACCGCTTCTCGTCTTACGATATGCGCGCTCCGATTCGC 1140
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Db 1081 TTGGGCGGGAATGGGCTGACCGCTTCTCGTCTTACGATATGCGCGCTCCGATTCGC 1140
OY 1141 AGCGATGCGCTTCTATGCGCTTCTGAGAGTTCCTGAGTTTAAACAGACCAACAG 1200
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OY 1741 AAGCTCTAGGCGCCCGGAACACGAGGAGCTGTTTCTTTGAATAACAGATATATCC 1800
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Db 1741 AAGCTCTAGGCGCCCGGAACACGAGGAGCTGTTTCTTTGAATAACAGATATATCC 1800
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Db 1801 AAGGGGCTTATAGGCGCTACTGCCAACAAGCGGAGGCTACTTGGCTGATATAGT 1860
OY 1861 AAGCTCTAGGCGCGGAGACAGGAACAGGTGAGGGGAGGTCCAGGTGCTCCACCGCA 1920
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Db 1861 AAGCTCTAGGCGCGGAGACAGGAACAGGTGAGGGGAGGTCCAGGTGCTCCACCGCA 1920
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Db 2161 GGCAGAGCAGGGGAGGAGCTACTCTCCAGGCGCGTCTCCTACTTGAAGGCTCTTG 2220
OY 2221 GGCAGCTCGGACCTTACTTGTGTGTACAGAGCATGCCGATCTTCGGTGGCGCGCG 2280
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Db 2221 GGCAGCTCGGACCTTACTTGTGTGTGTACAGAGCATGCCGATCTTCGGTGGCGCGCG 2280
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OY 2461 GCGCAAGGATTAAGGTCTGTCTGTAACCCGCTCCGCGCAACCTTGAAGTTTCGCG 2520
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Db 3001 ATACCACTAGCGGAGAGCTATGTCTGTGTAGCAACGAGCGCTATATGACGCGCTTACC 3060
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Db 3121 CTGGACCCGACCTTACCATTTGAGACGACGACCGTGCACAAAGCGGGTGCAGCTCG 3180
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Db 3181 CAGCGGCGAGGAGAGCTGTAGGGGAGATGGGCAATTTACAGTTTGTGACTCCAGA 3240
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QY 5281 GCTAAGGTAGGGTGGCCAGGGGATCTCCCCCTCTCTGGCCAGCTCATCAGCTAGCCAG 5340
Db 5281 GCTAAGGTAGGGTGGCCAGGGGATCTCCCCCTCTCTGGCCAGCTCATCAGCTAGCCAG 5340
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QY 6661 ACGGTCACTGAGATGACATCCGTGTGAGAGTCAATCTACCAATGTTGTACTGGCC 6720
Db 6661 ACGGTCACTGAGATGACATCCGTGTGAGAGTCAATCTACCAATGTTGTACTGGCC 6720
QY 6721 CCCGAAGCCAGACAGGCGCATTAAGGTGCGCTCAGAGAGCGGCTTACATCGGGGGCCCCG 6780
Db 6721 CCCGAAGCCAGACAGGCGCATTAAGGTGCGCTCAGAGAGCGGCTTACATCGGGGGCCCCG 6780
QY 6781 ACTAATTTCTAAAGGAGAGACTGCGGCTATCGCGGTGCGCGAGCGGCTGACTAGAG 6840
Db 6781 ACTAATTTCTAAAGGAGAGACTGCGGCTATCGCGGTGCGCGAGCGGCTGACTAGAG 6840
QY 6841 ACCAGCTGCGGTATTAACCTCACAATTTACTTAAGGCGGCTGCGGCTGCGAGGTGG 6900
Db 6841 ACCAGCTGCGGTATTAACCTCACAATTTACTTAAGGCGGCTGCGGCTGCGAGGTGG 6900
QY 6901 AAGCTCCAGAGCTGACAGATGCTGTATGCGGAGAGAGACCTTGTCTTATCTGTGAAC 6960
Db 6901 AAGCTCCAGAGCTGACAGATGCTGTATGCGGAGAGAGACCTTGTCTTATCTGTGAAC 6960
QY 6961 GCGGGAGCCCAAGAGAGAGAGGAGGCTACGGGCTTCAAGGACTATGATTAATATC 7020
Db 6961 GCGGGAGCCCAAGAGAGAGAGGAGGCTACGGGCTTCAAGGACTATGATTAATATC 7020
QY 7021 TCTGCCCCCTTGGGAGACCCGCCCAACAGAAATAGACTGTGATTAATCATATC 7080
Db 7021 TCTGCCCCCTTGGGAGACCCGCCCAACAGAAATAGACTGTGATTAATCATATC 7080
QY 7081 TCCTCAATGTGTAGTGGGACAGATGATCTGTGCAAAAGGCTGTACTATCTACCCGT 7140
Db 7081 TCCTCAATGTGTAGTGGGACAGATGATCTGTGCAAAAGGCTGTACTATCTACCCGT 7140
QY 7141 GACCCACACACCCCTTGGCGGGGCTGCTGGGAGACACTGAGACACACTCCAGTCAAT 7200
Db 7141 GACCCACACACCCCTTGGCGGGGCTGCTGGGAGACACTGAGACACACTCCAGTCAAT 7200
QY 7201 TCTGTGAGGCAACATCATATGATATGCGCCACCTTGTGGCAAGATGATCTGTATG 7260
Db 7201 TCTGTGAGGCAACATCATATGATATGCGCCACCTTGTGGCAAGATGATCTGTATG 7260
QY 7261 ACTCATTTCTTCATCTCTTCTAGCTCAGGAGCAACATTTAAAAAGCCCTAGTTGTGAG 7320
Db 7261 ACTCATTTCTTCATCTCTTCTAGCTCAGGAGCAACATTTAAAAAGCCCTAGTTGTGAG 7320
QY 7321 ATTCAGGGGCGCTTATCTCATTTAGCCACCTTGAACCTACCTAGATCATTCAGACATC 7380
Db 7321 ATTCAGGGGCGCTTATCTCATTTAGCCACCTTGAACCTACCTAGATCATTCAGACATC 7380
QY 7381 CATGGCCTTACGCAATTTACATGATAGTACTCTCAGGTAGATCAATTAAGGGGCT 7440
Db 7381 CATGGCCTTACGCAATTTACATGATAGTACTCTCAGGTAGATCAATTAAGGGGCT 7440
QY 7441 TCATGCTCAGAGAACTTGGGTAACCGCCTTGAGAGTGTGAGAGATCGGGCCAGAAAT 7500
Db 7441 TCATGCTCAGAGAACTTGGGTAACCGCCTTGAGAGTGTGAGAGATCGGGCCAGAAAT 7500
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xx	The present invention provides protein and coding sequences from
cc	Hepatitis C virus (HCV), comprising all or part of the HCV genome and
cc	able to replicate efficiently when transcribed into a susceptible cell
cc	line without reducing the growth rate of the cell line by more than 10
cc	fold. The sequences are useful for screening for anti-HCV therapeutics,
cc	for detecting antibodies to HCV in a biological sample such as blood,
cc	serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
cc	for deriving authentic HCV components such as replication-complement
cc	non-infectious, replication-defective infection component, and
cc	replication defective non-infectious HCV, in gene therapy or gene
cc	vaccination targeted to hepatic tissue for treating an animal infected or
cc	susceptible to HCV infection and for studying HCV infection and
cc	propagation. The present sequence is a clone of a fragment of the HCV
cc	genome designated HCVR2.
xx	
S0	Sequence 7992 BP; 1648 A; 2368 C; 2243 G; 1733 T; 0 other:
Query Match	99.9%; Score 7980.8; DB 24; Length 7992;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 7985; Conservative	0; Mismatches 7; Indels 0; Gaps 0;
Qy	1 GCCAGCCCCCGATTGGGCGCAGCTCCACCATGATGACTCCCTGTGAGAATACTG 60
Db	1 GCCAGCCCCCGATTGGGCGCAGCTCCACCATGATGACTCCCTGTGAGAATACTG 60
Qy	61 TCTTTCACGCAAGAAAGCGCTACGCCATGGCGTTTAGTAGATGTCTGTGCACCCTCCAGGAC 120
Db	61 TCTTTCACGCAAGAAAGCGCTACGCCATGGCGTTTAGTAGATGTCTGTGCACCCTCCAGGAC 120
Qy	121 CCCCCCTCCCGGAGAGCCATAGTGCTGGGGAACCGGTAGATACCGGGAATTTCCAG 180
Db	121 CCCCCCTCCCGGAGAGCCATAGTGCTGGGGAACCGGTAGATACCGGGAATTTCCAG 180
Qy	181 GAGACCGGGGTCTTTCCTTGATCAACCCCGCTCAATCCCTGAGAATTTGGCGTGCCTCC 240
Db	181 GAGACCGGGGTCTTTCCTTGATCAACCCCGCTCAATCCCTGAGAATTTGGCGTGCCTCC 240
Qy	241 GCGAGACTGTGTACCCAGTAGTGTGTGGGTCCGAAAAGCCCTGTGTGATGCTCTGTATAG 300
Db	241 GCGAGACTGTGTACCCAGTAGTGTGTGGGTCCGAAAAGCCCTGTGTGATGCTCTGTATAG 300
Qy	301 GTGTGTGCGAGTGTCCCGGAGAGTCTGTCAACCGTCCACCATGAGAGCAATTCCTTAAC 360
Db	301 GTGTGTGCGAGTGTCCCGGAGAGTCTGTCAACCGTCCACCATGAGAGCAATTCCTTAAC 360
Qy	361 CTCAAAGAAAAACAAGAGGCGCCGATGATTTGAACAAGATGATTGACACGAGTCTC 420
Db	361 CTCAAAGAAAAACAAGAGGCGCCGATGATTTGAACAAGATGATTGACACGAGTCTC 420
Qy	421 CGGCGCGTGTGGTGGAGAGGCTATTCGGCTTTGACTGGGCAACAAGCAATGGGTGT 480
Db	421 CGGCGCGTGTGGTGGAGAGGCTATTCGGCTTTGACTGGGCAACAAGCAATGGGTGT 480
Qy	481 CTGATGCGCGGTGTTCGGCTGTACGCGCAGGAGGCGCCCGGTCTTTTGTCAAGACCG 540
Db	481 CTGATGCGCGGTGTTCGGCTGTACGCGCAGGAGGCGCCCGGTCTTTTGTCAAGACCG 540
Qy	541 ACCTGTCCGGTCCCTGATGAATGACAGAGAGGAGGAGGCGGCGCTATCGTGGCTGGCCA 600
Db	541 ACCTGTCCGGTCCCTGATGAATGACAGAGAGGAGGAGGCGGCGCTATCGTGGCTGGCCA 600
Qy	601 CGAGCGGCGTTCCTTGCAGCTGTGCTGCAGCTTGTACTGAAGCGGGAAGGAGACTGGC 660
Db	601 CGAGCGGCGTTCCTTGCAGCTGTGCTGCAGCTTGTACTGAAGCGGGAAGGAGACTGGC 660
Qy	661 TGCTATTGGGCGCAAGTGGCGGAGAGATTCCTGTATCTCACTGATGATCGGCTACCTGGC 720
Db	661 TGCTATTGGGCGCAAGTGGCGGAGAGATTCCTGTATCTCACTGATGATCGGCTACCTGGC 720
Qy	721 AAGTATCATCATGCTGATGCAATGGAGGAGCTGATACGCTTGATCGGCTACCTGGC 780
Db	721 AAGTATCATCATGCTGATGCAATGGAGGAGCTGATACGCTTGATCGGCTACCTGGC 780

QY	781	CATTGACCAACCAAGGAAACATCGCATCGACGACACAGTACTGGATGAGACCGGTC	840
Db	781	CATTGACCAACCAAGGAAACATCGCATCGACGACACAGTACTGGATGAGACCGGTC	840
QY	841	TTTGATGATGAGATGATGAGAGAGCATCAGAGGCGTCGCGCACCACTGTTCG	900
Db	841	TTTGATGATGAGATGATGAGAGAGCATCAGAGGCGTCGCGCACCACTGTTCG	900
QY	901	CCAGGCTCAAGCGCGCATGCCGACGCGGAGAGATCTGTCGTACCACTGGCATGCT	960
Db	901	CCAGGCTCAAGCGCGCATGCCGACGCGGAGAGATCTGTCGTACCACTGGCATGCT	960
QY	961	GCTTGGCAATATCATGATGATGAGAAATGGCCGCTTTTCTGATCATCATGTCGTCGCG	1020
Db	961	GCTTGGCAATATCATGATGAGAAATGGCCGCTTTTCTGATCATCATGTCGTCGCG	1020
QY	1021	TGGGTGTGGGGAGCCGCTATCAGAGACATAGCGTTGGCTAACCGCTATTTCTGAAGC	1080
Db	1021	TGGGTGTGGGGAGCCGCTATCAGAGACATAGCGTTGGCTAACCGCTATTTCTGAAGC	1080
QY	1081	TTGGCGGCGAATGGCGCTGACCGCTTCCTGATGCTTACGATTCGCGCCCTCCGATTCG	1140
Db	1081	TTGGCGGCGAATGGCGCTGACCGCTTCCTGATGCTTACGATTCGCGCCCTCCGATTCG	1140
QY	1141	AGCGCATGCGCTTCTATCGGCTCTTGAGAGTCTCTGAGATTAAACACACCAACG	1200
Db	1141	AGCGCATGCGCTTCTATCGGCTCTTGAGAGTCTCTGAGATTAAACACACCAACG	1200
QY	1201	GTTTCCCTCATAGCGGATCATTCGCGCCCTCTCCCTCCCGCCCGCCCTCAAGTACTGCG	1260
Db	1201	GTTTCCCTCATAGCGGATCATTCGCGCCCTCTCCCTCCCGCCCGCCCTCAAGTACTGCG	1260
QY	1261	CGAAGCGGCTTGGAATAAGCGCGGTGGTGTGCTATATGTTATTTTCCACATATG	1320
Db	1261	CGAAGCGGCTTGGAATAAGCGCGGTGGTGTGCTATATGTTATTTTCCACATATG	1320
QY	1321	CCGTCCTTTGGCAATGTAGAGGGCCCGGAAACCTGSCCCTGCTTTTGAAGCATTCCT	1380
Db	1321	CCGTCCTTTGGCAATGTAGAGGGCCCGGAAACCTGSCCCTGCTTTTGAAGCATTCCT	1380
QY	1381	AGGGTCTTCCCTCTCGCCCAAGAAGATGCAAGTCTTTAATAGTGTGAAGSAAACA	1440
Db	1381	AGGGTCTTCCCTCTCGCCCAAGAAGATGCAAGTCTTTAATAGTGTGAAGSAAACA	1440
QY	1441	GTTCTCTGGAAGCTTCTTGAAGACAACAACGTCGTAGACACCCCTTTCAGCAGCGG	1500
Db	1441	GTTCTCTGGAAGCTTCTTGAAGACAACAACGTCGTAGACACCCCTTTCAGCAGCGG	1500
QY	1501	AACCCCCCACTGGCGACAGGTGCTCTGGGGGCCAAACACCGTGTAAAGATACCT	1560
Db	1501	AACCCCCCACTGGCGACAGGTGCTCTGGGGGCCAAACACCGTGTAAAGATACCT	1560
QY	1561	GCAAAAGCGGACACACCCACAGTGCACAGTTGTAGTGGATGTGTGAAAAGATCAA	1620
Db	1561	GCAAAAGCGGACACACCCACAGTGCACAGTTGTAGTGGATGTGTGAAAAGATCAA	1620
QY	1621	TGGCTCTCTCAACGATATTCACAAGAGGGCTAAAGATAGCCACAGAAGTACCATTGT	1680
Db	1621	TGGCTCTCTCAACGATATTCACAAGAGGGCTAAAGATAGCCACAGAAGTACCATTGT	1680
QY	1681	ATGGGATCTGATCTGGGAGCTCGGTGCATGCTTTACATGTGTATTAGTCAGGTTAAA	1740
Db	1681	ATGGGATCTGATCTGGGAGCTCGGTGCATGCTTTACATGTGTATTAGTCAGGTTAAA	1740
QY	1741	AACGCTCTAGGCCCCCGACACAGAGGGAGCATGTCTTCTTGGAAAAACACATATAC	1800
Db	1741	AACGCTCTAGGCCCCCGACACAGAGGGAGCATGTCTTCTTGGAAAAACACATATAC	1800
QY	1801	ATGGCGCTATTACGGCTACTCCACAAGACGCGAGGCTTACTGTGATCATCTACT	1860
Db	1801	ATGGCGCTATTACGGCTACTCCACAAGACGCGAGGCTTACTGTGATCATCTACT	1860

QY	1861	AGCCTCACAGCCCGGAGCAGAAACACAGGTCCAGAGGGAGACTCCAGTGTCTCCACCGCA	1920
Db	1861	AGCCTCACAGCCCGGAGCAGAAACACAGGTCCAGAGGGAGACTCCAGTGTCTCCACCGCA	1920
QY	1921	ACACAATCTTCTCGGGGAGACTCGTCAATGGCGTGTGGAGCTGTATCATGTGTCC	1980
Db	1921	ACACAATCTTCTCGGGGAGACTCGTCAATGGCGTGTGGAGCTGTATCATGTGTCC	1980
QY	1981	GGCTCAAGACCTTGTGCGGCGCCAAAGGGCCCATTCACCAATGTACACCAATGTGGAC	2040
Db	1981	GGCTCAAGACCTTGTGCGGCGCCAAAGGGCCCATTCACCAATGTACACCAATGTGGAC	2040
QY	2041	CAGAGCCTCGTGGCTGGCAAGCGCCCGCGGGGCGCTTCTTGCACACATGCACCTGC	2100
Db	2041	CAGAGCCTCGTGGCTGGCAAGCGCCCGCGGGGCGCTTCTTGCACACATGCACCTGC	2100
QY	2101	GGCAGCTCGGACTTTTACTTGGTACAGAGGCATCCGATGTATTCGGTGCCGCGCGG	2160
Db	2101	GGCAGCTCGGACTTTTACTTGGTACAGAGGCATCCGATGTATTCGGTGCCGCGCGG	2160
QY	2161	GGCAGCAGCAGGGGAGGACTACTCTCCCGAGGCGCGTCTCTACTTGAAGAGGCTCTCG	2220
Db	2161	GGCAGCAGCAGGGGAGGACTACTCTCCCGAGGCGCGTCTCTACTTGAAGAGGCTCTCG	2220
QY	2221	GGCGGTCCACTGTCTGCTGCGGCGGACGCTGTGGGCATCTTTCGGGCTGCGTGTGC	2280
Db	2221	GGCGGTCCACTGTCTGCTGCGGCGGACGCTGTGGGCATCTTTCGGGCTGCGTGTGC	2280
QY	2281	ACCCGAGGGGTTGGGAGAGCGGTGTGTATCCCGTGGAGCTATGGAAACCACTATG	2340
Db	2281	ACCCGAGGGGTTGGGAGAGCGGTGTGTATCCCGTGGAGCTATGGAAACCACTATG	2340
QY	2341	CGGTCCCGGCTTCCAGGACAACTGCTCCCTCGCGCGGTACCGGACATTCAGAGTG	2400
Db	2341	CGGTCCCGGCTTCCAGGACAACTGCTCCCTCGCGCGGTACCGGACATTCAGAGTG	2400
QY	2401	GCCCATCTACACGCCCTTACTGTGTACGCGCAAGACCTAAGGTGCGGCTGCTGTATGCA	2460
Db	2401	GCCCATCTACACGCCCTTACTGTGTACGCGCAAGACCTAAGGTGCGGCTGCTGTATGCA	2460
QY	2461	GCCCAAGGGTTAAGAGGTGTGTCTCAACCGTTCGTGGCGCCACCCCTAGTGTCCGG	2520
Db	2461	GCCCAAGGGTTAAGAGGTGTGTCTCAACCGTTCGTGGCGCCACCCCTAGTGTCCGG	2520
QY	2521	GCGTATGTGTAAAGGCACATGTATGCACCTAACATCAGAACCGGGTTAAGGACATC	2580
Db	2521	GCGTATGTGTAAAGGCACATGTATGCACCTAACATCAGAACCGGGTTAAGGACATC	2580
QY	2581	ACCAAGGGTGGCCCCATTCAGTACTCCACTATGGCAAGTTCTTTCGACAGGTGGTGC	2640
Db	2581	ACCAAGGGTGGCCCCATTCAGTACTCCACTATGGCAAGTTCTTTCGACAGGTGGTGC	2640
QY	2641	TCTGAGGCGGCTATGACATCATATATGTGATGAGTGGCCACTCACTACTCGACACT	2700
Db	2641	TCTGAGGCGGCTATGACATCATATATGTGATGAGTGGCCACTCACTACTCGACACT	2700
QY	2701	ATCTGGGCATTCGGACATGCTCTGTGACCAAGCGAGACGAGCTGAGCCGACTCGTCTG	2760
Db	2701	ATCTGGGCATTCGGACATGCTCTGTGACCAAGCGAGACGAGCTGAGCCGACTCGTCTG	2760
QY	2761	CTGCGCACCGGTAGCGCTCCGGGATCGGTACCGTGTGCACATTCCAAAACATTCGAGAGTG	2820
Db	2761	CTGCGCACCGGTAGCGCTCCGGGATCGGTACCGTGTGCACATTCCAAAACATTCGAGAGTG	2820
QY	2821	GCTCTGTCCAGCTGTGAGAAATCCCTTTATGTGCAAAAGCCATCCCATTCGAGACATC	2880
Db	2821	GCTCTGTCCAGCTGTGAGAAATCCCTTTATGTGCAAAAGCCATCCCATTCGAGACATC	2880
QY	2881	AAGGGGGGAGGACACACTATTTTGTGCATTCCAAGAAAGAAATGATATGAGCTGCGCGG	2940
Db	2881	AAGGGGGGAGGACACACTATTTTGTGCATTCCAAGAAAGAAATGATATGAGCTGCGCGG	2940
QY	2941	AAGCTGTCCGCGCTCGACACTCAATGTGTGTAGCAATATTACCGGGGCGCTTATGTATTCGTC	3000

Db 2941 AAGCTGTCCGGCTCGGACTAATGCTGTAGCATATTACCGGGCCCTTGATGATCCGTC 3000
QY 3001 ATACCAACTAGCGAGAGATGCTATTTGCTAGCAACGAGCGCTTAATAGAGGGCTTTACC 3060
Db 3001 ATACCAACTAGCGAGAGATGCTATTTGCTAGCAACGAGCGCTTAATAGAGGGCTTTACC 3060
QY 3061 GGGGATTTGACTCAGTATGACTGCAATACATGTGTCAACCGACAGATGCTAGC 3120
Db 3061 GGGGATTTGACTCAGTATGACTGCAATACATGTGTCAACCGACAGATGCTAGC 3120
QY 3121 CTGAGCCGACCTTACCATTTAGAGAGAGACCGTGCACAGAGAGCGGTGTACGCTCG 3180
Db 3121 CTGAGCCGACCTTACCATTTAGAGAGAGACCGTGCACAGAGAGCGGTGTACGCTCG 3180
QY 3181 CAGCGGCGAGAGAGAGATGTAAGGGAGAGATGGGCAATTTACAGGTTGTGACTCCAGGA 3240
Db 3181 CAGCGGCGAGAGAGAGATGTAAGGGAGAGATGGGCAATTTACAGGTTGTGACTCCAGGA 3240
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Db 3301 GCTTGTGACAGAGCTACGCCCGGAGAGCTCAGTTAGGTTGCGGGCTTACTTAACACA 3360
QY 3361 CCAGGGTTAGCCGCTGTGCGAGAGCATGTGAGTTCTGGGAGAGCGTCTTACAGGCGCTC 3420
Db 3361 CCAGGGTTAGCCGCTGTGCGAGAGCATGTGAGTTCTGGGAGAGCGTCTTACAGGCGCTC 3420
QY 3421 ACCCAATAGAGCGCCCATTTCTTGTCTCCAGACTAGAGAGGAGAGACAATTCCTCCCTAC 3480
Db 3421 ACCCAATAGAGCGCCCATTTCTTGTCTCCAGACTAGAGAGGAGAGACAATTCCTCCCTAC 3480
QY 3481 CTGAGAGATACAGGCTACGGTGTGCGGAGAGGCTCAGGCTCCACCTCATGCTGGAGC 3540
Db 3481 CTGAGAGATACAGGCTACGGTGTGCGGAGAGGCTCAGGCTCCACCTCATGCTGGAGC 3540
QY 3541 CAATGTGGAAGTGTCTATAGCGCTAAAGCGCTACGCTGCAAGCGGCCAACGCCCTGCTG 3600
Db 3541 CAATGTGGAAGTGTCTATAGCGCTAAAGCGCTACGCTGCAAGCGGCCAACGCCCTGCTG 3600
QY 3601 TATAGGCTGAGGCGGCTCAAAAGAGGTACTACACAGCCCATTAACCAATATATC 3660
Db 3601 TATAGGCTGAGGCGGCTCAAAAGAGGTACTACACAGCCCATTAACCAATATATC 3660
QY 3661 ATGCGATGATGTGCGCTGACCTGAGGTGCTACAGAGCACCTGGTGTGTAAGCGGA 3720
Db 3661 ATGCGATGATGTGCGCTGACCTGAGGTGCTACAGAGCACCTGGTGTGTAAGCGGA 3720
QY 3721 GTCTAGAGAGCTGTGCGCGGATTTGCTGACAAAGAGAGCGGTGCTATTTGGGAGG 3780
Db 3721 GTCTAGAGAGCTGTGCGCGGATTTGCTGACAAAGAGAGCGGTGCTATTTGGGAGG 3780
QY 3781 ATCATCTTGTCCGGAAGCGCGCATCATCTCCGACAGGAGAGTCTTTACCGGAGATTC 3840
Db 3781 ATCATCTTGTCCGGAAGCGCGCATCATCTCCGACAGGAGAGTCTTTACCGGAGATTC 3840
QY 3841 GATGAGATGGAAGTGTGCGGCTCACACTCCCTTACATCGAAGGGAATGTGACGCTGCC 3900
Db 3841 GATGAGATGGAAGTGTGCGGCTCACACTCCCTTACATCGAAGGGAATGTGACGCTGCC 3900
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Db 3901 GAACATTTCAACAGAGAGCATGCGGTTGCTGCAAAAGAGAGAGAGAGAGAGAGCT 3960
QY 3961 GCTGCTCCGCTGTGGAATCCAAGTGGCGAGACCTCGAAGCTTTCTGGGAGAAACATATG 4020
Db 3961 GCTGCTCCGCTGTGGAATCCAAGTGGCGAGACCTCGAAGCTTTCTGGGAGAAACATATG 4020
QY 4021 TGAATTTTCAATAGCGGATACAAATATTAGAGGCTTGTCACTGCTGGAACCC 4080
Db 4021 TGAATTTTCAATAGCGGATACAAATATTAGAGGCTTGTCACTGCTGGAACCC 4080
Db 4081 GCGATAGCATAGATGATGATGATACAGCCCTTATCAACAGCCGCTACACAGCAACAT 4140
QY 4081 GCGATAGCATAGATGATGATGATACAGCCCTTATCAACAGCCGCTACACAGCAACAT 4140
Db 4081 GCGATAGCATAGATGATGATGATACAGCCCTTATCAACAGCCGCTACACAGCAACAT 4140
QY 4141 ACCCTCTGTTTACATCTTGGGGGATGGTGGCCGCCCACTTGTCTCTCCAGCGCT 4200
Db 4141 ACCCTCTGTTTACATCTTGGGGGATGGTGGCCGCCCACTTGTCTCTCTCCAGCGCT 4200
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Db 4201 GCTTGTGCTTGTAGAGCGCGGATGCTGAGAGCGGCTGTGAGACATAGAGCTTGGG 4260
QY 4261 AAGTGCTTGTGATATTGTTGGCAGTTATGAGACAGGGGTGGCAGCGCGCTGTGGCC 4320
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QY 4441 GTGGGCGGAGGAGGAGGCTGTGAGTGTGAGACCGGCTGATAGGCTTGTGGCGG 4500
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QY 4501 GGTAAACAGCTGTCCCGCAGCACTATGTGCTGAGAGCAGAGCTGACAGCAGTGTCACT 4560
Db 4501 GGTAAACAGAGCTGTCCCGCAGCACTATGTGCTGAGAGCAGAGCTGACAGCAGTGTCACT 4560
QY 4561 CAGATCTCTGAGTGTACCATCAGTGTGAGAGGCTGACAGGCTGACAGGCTGAGTCAAC 4620
Db 4561 CAGATCTCTGAGTGTACCATCAGTGTGAGAGGCTGACAGGCTGACAGGCTGAGTCAAC 4620
QY 4621 GAGGACTCTCCAGCGCATGCTCGGCTCGTGGCTAAGAGATGTTGGATGGATATGC 4680
Db 4621 GAGGACTCTCCAGCGCATGCTCGGCTCGTGGCTAAGAGATGTTGGATGGATATGC 4680
QY 4681 ACAGTGTGATGATTTAAAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 4740
Db 4681 ACAGTGTGATGATTTAAAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 4740
QY 4741 GTCCCTTCTTCTCATGTCAACGTGGGTACAAGGAGTGTGCGGGGAGAGGCAATCATG 4800
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Db 4801 CAACACACCTGCGCATGTGAGAGCAGATCACCGAGATGTGAAAAAGGTTCCATGAG 4860
QY 4861 ATCTGTGGGCTTAGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACGCGTAC 4920
Db 4861 ATCTGTGGGCTTAGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACGCGTAC 4920
QY 4921 ACCAGGGGCGCTGAGCGCCCTCCCGGCGCAATTAATCTGAGGGGCTGTGGCGGCTG 4980
Db 4921 ACCAGGGGCGCTGAGCGCCCTCCCGGCGCAATTAATCTGAGGGGCTGTGGCGGCTG 4980
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Db 5041 ACCACTGACAAAGTAAATGCGCTGTGAGATTTCCAGTTCCGCGCCCAATTTCTTCAAGAAATG 5100
QY 5101 GATGGGCTGCTGAGAGTACAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 5160
Db 5101 GATGGGCTGCTGAGAGTACAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 5160

QY 5161 ACATTCTGTGGGGCTCAATCAATACCTGGTTGGGTGCACAGCTCCCATCGAGCCCGAA 5220
DB 5161 ACATTCTGTGGGGCTCAATCAATACCTGGTTGGGTGCACAGCTCCCATCGAGCCCGAA 5220
QY 5221 CCGAGCTAGAGTGTCTACTCTCATCTCCACGACCCCTCCACATTACGGCGAGAG 5280
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DB 5401 TCAGAAATTAAGTGTAGTATTTTGGACTCTTGAGCGCGCTCCAGCGGAGGAGGATGAG 5520
QY 5461 TCAGAAATTAAGTGTAGTATTTTGGACTCTTGAGCGCGCTCCAGCGGAGGAGGATGAG 5520
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DB 5521 AAGGAGTATCCGTTCCGCGGAGAGTCTGCGAGAGTCCAGGAAATTCCTCGAGCGATG 5580
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DB 5581 CCCATATGGGACGCCCGGATTTACAACTCCATGTTAGTCTTGGAGGAGAGCCGAG 5640
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QY 5761 GAGCTGGCCAAAGACCTTCGCGAGTCCGATCTGTCGCGCGTCGACAGGCGACGCGA 5820
DB 5761 GAGCTGGCCAAAGACCTTCGCGAGTCCGATCTGTCGCGCGTCGACAGGCGACGCGA 5820
QY 5821 ACGGCTCTCTGACACGCGCTCGAGAGCGCGACGCGGATCCGAGCTTGAATGCTGAC 5880
DB 5821 ACGGCTCTCTGACACGCGCTCGAGAGCGCGACGCGGATCCGAGCTTGAATGCTGAC 5880
QY 5881 TCTCCATGCCCCCTTGGAGGGGAGCGGGGGATCCGATCTCAGGAGAGGGTCTTGG 5940
DB 5881 TCTCCATGCCCCCTTGGAGGGGAGCGGGGGATCCGATCTCAGGAGAGGGTCTTGG 5940
QY 5941 TCTACCGTAAGCAGAGAGGCTAGTGAAGACGTGCTGCTCTCGATGCTCTACACATGG 6000
DB 5941 TCTACCGTAAGCAGAGAGGCTAGTGAAGACGTGCTGCTCTCGATGCTCTACACATGG 6000
QY 6001 AAGAGGCGCCCTATCAGCGCATGCGCTGGGAGGAAACCAAGCGCCCATAAATGCACTG 6060
DB 6001 AAGAGGCGCCCTATCAGCGCATGCGCTGGGAGGAAACCAAGCGCCCATAAATGCACTG 6060
QY 6061 AAGCACTCTTGTCTCGTCACCAACTGTGTATGCTAGACACATCTCGAGCGCAAGC 6120
DB 6061 AAGCACTCTTGTCTCGTCACCAACTGTGTATGCTAGACACATCTCGAGCGCAAGC 6120
QY 6121 CTGCGGAGAGAGGTGACCTTTGACAGACTGACAGTCTCGAGAGACCATACCGGAG 6180
DB 6121 CTGCGGAGAGAGGTGACCTTTGACAGACTGACAGTCTCGAGAGACCATACCGGAG 6180
QY 6181 GTGCTCAGAGAGATGAAGGCGAAGGGCTCCAGAGTTAAGGGCTTAATCTCTATCCGTGAG 6240
DB 6181 GTGCTCAGAGAGATGAAGGCGAAGGGCTCCAGAGTTAAGGGCTTAATCTCTATCCGTGAG 6240

QY 6241 GAAGCTCTAGACTGACGCCCCACATTCGGCCAGATCTAATTTGCTATGGGCGAAG 6300
DB 6241 GAAGCTCTAGACTGACGCCCCACATTCGGCCAGATCTAATTTGCTATGGGCGAAG 6300
QY 6301 GACGTCCGGAACCTATCCAGCAGAGCGGTTAACCACATCCGCTCCGTGTGGAAAGACTTG 6360
DB 6301 GACGTCCGGAACCTATCCAGCAGAGCGGTTAACCACATCCGCTCCGTGTGGAAAGACTTG 6360
QY 6361 CTGGAAGACTGAGACACCAATGACACCACTCATGCGCAAAAATGAGTGTCTGC 6420
DB 6361 CTGGAAGACTGAGACACCAATGACACCACTCATGCGCAAAAATGAGTGTCTGC 6420
QY 6421 GTCCAAACGAGAAAGGGGGCCGAGACCACTGCGCTTATCGATTCCAGATTGGG 6480
DB 6421 GTCCAAACGAGAAAGGGGGCCGAGACCACTGCGCTTATCGATTCCAGATTGGG 6480
QY 6481 GTTCGTGTGTGCGAAGAAATGGCCCTTAGATGTGTCTCAAGCCCTCCAGCGCGTG 6540
DB 6481 GTTCGTGTGTGCGAAGAAATGGCCCTTAGATGTGTCTCAAGCCCTCCAGCGCGTG 6540
QY 6541 ATGGGCTTTCATACGGAATTCGAATCTCTCTGAGACAGCGGGTCAAGTTCTGTGAT 6600
DB 6541 ATGGGCTTTCATACGGAATTCGAATCTCTCTGAGACAGCGGGTCAAGTTCTGTGAT 6600
QY 6601 GCCTGAAAGCAGAAATGCGCTATGGGCTTCGATATGACACCCGCTGTTTGACTCA 6660
DB 6601 GCCTGAAAGCAGAAATGCGCTATGGGCTTCGATATGACACCCGCTGTTTGACTCA 6660
QY 6661 ACGGTCACTGAGAAATGACATCCGTGTGAGAGTCAATCTCAATTTGTGACTTGGCC 6720
DB 6661 ACGGTCACTGAGAAATGACATCCGTGTGAGAGTCAATCTCAATTTGTGACTTGGCC 6720
QY 6721 CCCGAAAGCCAGACGCCCTAATAGTCTGCTACAGAGCGGCTTTACATCGGGGGCCCTG 6780
DB 6721 CCCGAAAGCCAGACGCCCTAATAGTCTGCTACAGAGCGGCTTTACATCGGGGGCCCTG 6780
QY 6781 ACTAATTTAAAGGCGAGACATCGCGGCTATGCGCGGAGCGCGAGCGGTTACTGACG 6840
DB 6781 ACTAATTTAAAGGCGAGACATCGCGGCTATGCGCGGAGCGCGAGCGGTTACTGACG 6840
QY 6841 ACCAGCTGGGTAATACCTGACATGTTACTTGAAGGCGCGCTGCGAGCTGCG 6900
DB 6841 ACCAGCTGGGTAATACCTGACATGTTACTTGAAGGCGCGCTGCGAGCTGCG 6900
QY 6901 AAGCTCCAGAGTGCACATGCTGTATGCGGAGACGCTTGCATTATCTGGAAGC 6960
DB 6901 AAGCTCCAGAGTGCACATGCTGTATGCGGAGACGCTTGCATTATCTGGAAGC 6960
QY 6961 GCGGGGACCCAGAGAGAGAGCGAGCGCTACGCGGCTTCAAGGAGCTATGACTGATAC 7020
DB 6961 GCGGGGACCCAGAGAGAGAGCGAGCGCTACGCGGCTTCAAGGAGCTATGACTGATAC 7020
QY 7021 TCTGCCCCCTGCGGAGACCGCGCAACCAATACGACTGGAATGATTAATCATGTC 7080
DB 7021 TCTGCCCCCTGCGGAGACCGCGCAACCAATACGACTGGAATGATTAATCATGTC 7080
QY 7081 TCTCCATATGTGTACGTGCGGACGATCATGTGCAAAAAGGTTACTATCTACCCGT 7140
DB 7081 TCTCCATATGTGTACGTGCGGACGATCATGTGCAAAAAGGTTACTATCTACCCGT 7140
QY 7141 GACCCACACACCCCTTGGCGGGCTGCGTGGAGAGAGCTAGACACTCCAGTCAAT 7200
DB 7141 GACCCACACACCCCTTGGCGGGCTGCGTGGAGAGAGCTAGACACTCCAGTCAAT 7200
QY 7201 TCTGCTAGGACATCATCTATGATGCGCCACCTTGTGGGAAAGGATGATCTGATG 7260
DB 7201 TCTGCTAGGACATCATCTATGATGCGCCACCTTGTGGGAAAGGATGATCTGATG 7260
QY 7261 ACTCATTTTCTTCCATCTTACGTAGAGAAACACTTGAAAAAGCCCTGATTTGACG 7320
DB 7261 ACTCATTTTCTTCCATCTTACGTAGAGAAACACTTGAAAAAGCCCTGATTTGACG 7320
QY 7321 ATCTAGGGGCGCTGTACTCATGAGCCACTTGACCTACCTGATCATCAAGCACTC 7380

XX Bichko V.;
DR WEI; 2002-490082/52.
PT Novel nucleic acid encoding replication competent recombinant hepatitis
FT C virus genome useful for screening anti-hepatitis C virus therapeutics
PS and for vaccine development
XX Claim 10; Page 66-70; 85bp; English.

xx The present invention provides protein and coding sequences from
cc Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject
CC for deriving authentic HCV components such as replication-complement
CC non-infectious, replication-defective infection-component, and
CC replication-defective non-infectious HCV, in gene therapy or gene
CC vaccination targeted to hepatic tissue for treating an animal infected or
CC susceptible to HCV infection and for studying HCV infection and
CC propagation. The present sequence is a clone of a fragment of the HCV
CC genome designated HCVR22.

SQ Sequence 7992 BP; 1646 A; 2368 C; 2245 G; 1733 T; 0 other:

Query Match Best Local Similarity 99.9%; Score 7980.8; DB 24; Length 7992;
Matches 7989; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTTGGGSGCAGACTCCACCATAGATCACTCCCCTGTGAGAACTACTG 60
Db 1 GCCAGCCCCCGATTTGGGSGCGACACTCCACCATAGATCACTCCCCTGTGAGAACTACTG 60

OY 61 TCCTCAGCAGGAAGAAGCGCTTACGCATGGGGTAGTAGTGAGTGTGCGTGCACGCTCCAGAGAC 120
Db 61 TCCTCAGCAGGAAGAAGCGCTTACGCATGGGGTAGTAGTGAGTGTGCGTGCACGCTCCAGAGAC 120

OY 121 CCCCCCTCCCGGAGAACCATAGTGTCTGGGGAACCGGTGAGTACACC GGAAATTGCCAG 180
Db 121 CCCCCCTCCCGGAGAGACCATAGTGTCTGGGGAACCGGTGAGTACACC GGAAATTGCCAG 180

OY 181 GAGCACCGGSGTCTTTCTTTGTGATCAACCGGTCATGGCTGGAATTTGGGCGTGGCCCC 240
Db 181 GAGCACCGGSGTCTTTCTTTGTGATCAACCGGTCATGGCTGGAATTTGGGCGTGGCCCC 240

OY 241 GCGAGACTGCTAGCCGAGTAGTGTGGTGGCGGAAAGGCTTTGTGTACTGCTGATAGG 300
Db 241 GCGAGACTGCTAGCCGAGTAGTGTGGTGGCGGAAAGGCTTTGTGTACTGCTGATAGG 300

OY 301 GTGGTTTCGAGTSCCCCGGGAGGTCTCGTAGACCGTGGACCATGAGACCAATCTATAAC 360
Db 301 GTGGTTTCGAGTSCCCCGGGAGGTCTCGTAGACCGTGGACCATGAGACCAATCTATAAC 360

OY 361 CTCAGAAAAAACCAGAGGGCGGCCATGATTGAACAAGATGATTCAGACGAGTTCTC 420
Db 361 CTCAGAAAAAACCAGAGGGCGGCCATGATTGAACAAGATGATTCAGACGAGTTCTC 420

OY 421 CGGCGCGTGGGTGAGAGAGCTATTGCGCTATGACTGTGGGCAACAACATCATGCGTGTCT 480
Db 421 CGGCGCGTGGGTGAGAGAGCTATTGCGCTATGACTGTGGGCAACAACATCATGCGTGTCT 480

OY 481 CTGATGCCGCCGTGTTCCGAGCTGTCAAGCGCAGGGGCGCCGCTTTTGTCTAAGACCG 540
Db 481 CTGATGCCGCCGTGTTCCGAGCTGTCAAGCGCAGGGGCGCCGCTTTTGTCTAAGACCG 540

OY 541 ACCTGTCGGGTGCCCTGAATGAATGCAAGAGCAGAGCCGCGCTATCTGTCGTGGCCA 600
Db 541 ACCTGTCGGGTGCCCTGAATGAATGCAAGAGCAGAGCCGCGCTATCTGTCGTGGCCA 600

OY 601 CGACGGGCGTTCCTGTGCGAGCTGTCTGAGACTTGTCACTGAAGCGGAAAGGACTGCG 660
Db 601 CGACGGGCGTTCCTGTGCGAGCTGTCTGAGACTTGTCACTGAAGCGGAAAGGACTGCG 660

Db	601	CGAGGGGCGTTTCCTTCTGCGAGCGCTGTGCTGAGCGTGTGTCTACGTAAGCGGGAAGGAGCTAGCG	660
Qy	661	TGCTATTGGGCGAAGTCCGGGGGCGAAGATCCTCTCTACTCTACCTTGTCTCTCTCCGCGAGA	720
Db	661	TGCTATTGGGCGAAGTCCGGGGGCGAAGATCCTCTCTACTCTACCTTGTCTCTCTCCGCGAGA	720
Qy	721	AAGTATCCATCATAGCTGAGTGCATAATGCGCGGCTGCATACGCTTGATCCGGCTTACCTGCC	780
Db	721	AAGTATCCATCATAGCTGAGTGCATAATGCGCGGCTGCATACGCTTGATCCGGCTTACCTGCC	780
Qy	841	TTTGTCATCAGATGATCTGTGACGAAGAGCATCAGGGGCTGCGCGCAGACGCACTGTTTCG	900
Db	841	TTTGTCATCAGATGATCTGTGACGAAGAGCATCAGGGGCTGCGCGCAGACGCACTGTTTCG	900
Qy	901	CCAGGCTCAAGGGGCGCATAGCCCGACGCGGAGAGATCTGTGTGACCCATGGCCATGCT	960
Db	901	CCAGGCTCAAGGGGCGCGCATAGCCCGACGCGGAGAGATCTGTGTGACCCATGGCCATGCT	960
Qy	1021	TGGGTGTGGGGGACCGCTATACAGAGATAGCGTGTGACCGGTATATTTCTCTAGAGAGC	1080
Db	1021	TGGGTGTGGGGGACCGCTATACAGAGATAGCGTGTGACCGGTATATTTCTCTAGAGAGC	1080
Qy	1081	TTGCGGGCGAATGAGGCTGACCGCTTCTCTGTGCTTTAGCGTATGCGCGCTCCGATTTGC	1140
Db	1081	TTGCGGGCGAATGAGGCTGACCGCTTCTCTGTGCTTTAGCGTATGCGCGCTCCGATTTGC	1140
Qy	1141	AGGCGATCGGCTTCTATCGGCTCTTGACGAGTCTCTGATTTAAACAACACACAAGC	1200
Db	1141	AGGCGATCGGCTTCTATCGGCTCTTGACGAGTCTCTGATTTAAACAACACACAAGC	1200
Qy	1201	GTTTCCCTTAGCGGGATCAATTCCGCGCCCTCTCCCTCCCGCCCTTACGTTACTGTGC	1260
Db	1201	GTTTCCCTTAGCGGGATCAATTCCGCGCCCTCTCCCTCCCGCCCTTACGTTACTGTGC	1260
Qy	1261	CGAAGCGCTGTGAATAGGCGCGGTGTGGTGTCTATATGTATTTTCCACATATTC	1320
Db	1261	CGAAGCGCTGTGAATAGGCGCGGTGTGGTGTCTATATGTATTTTCCACATATTC	1320
Qy	1321	CCGTCTTTTGGCAATGTGAAGGCGCCGGAACCTGCGCCCTGTCTTTTGAAGACATTTCT	1380
Db	1321	CCGTCTTTTGGCAATGTGAAGGCGCCGGAACCTGCGCCCTGTCTTTTGAAGACATTTCT	1380
Qy	1381	AGGGGTCTTCCCTCTCGCGCAAGAGATGCAAGGTCTGTAAATGTGTGAAGGAACA	1440
Db	1381	AGGGGTCTTCCCTCTCGCGCAAGAGATGCAAGGTCTGTAAATGTGTGAAGGAACA	1440
Qy	1441	GTTCTCTGGAAGCTTTTTAAGACAAACAAGCTCTGTAGCAACCTTTGACAGCGACGG	1500
Db	1441	GTTCTCTGGAAGCTTTTTAAGACAAACAAGCTCTGTAGCAACCTTTGACAGCGACGG	1500
Qy	1501	AACCCGCCACTGTGCGACAGGTGCCTGTGCGGCAAAACCCACAGTGTATAGATACACT	1560
Db	1501	AACCCGCCACTGTGCGACAGGTGCCTGTGCGGCAAAACCCACAGTGTATAGATACACT	1560
Qy	1561	GCAAGGCGGCAACAACCCACAGTGCCTGTGTAGTGTGATAGTTGTGGAAGAGTCAAA	1620
Db	1561	GCAAGGCGGCAACAACCCACAGTGCCTGTGTAGTGTGATAGTTGTGGAAGAGTCAAA	1620
Qy	1621	TGGCTCTCTCAACCGTATTTCAACAAGGGGCTGAAGAGTGCACAGAGGTACCCCATGT	1680
Db	1621	TGGCTCTCTCAACCGTATTTCAACAAGGGGCTGAAGAGTGCACAGAGGTACCCCATGT	1680
Qy	1681	ATGGGATCTGATCTGGGGGCTCGGTGTGACATGCTTTACATAGTTTGAAGCGAGTTAAA	1740
Db	1681	ATGGGATCTGATCTGGGGGCTCGGTGTGACATGCTTTACATAGTTTGAAGCGAGTTAAA	1740

QY	1741	AACTGTAGGCCCCCGAAACACAGCGGAGCTGTTTCTTCTTGA AAAACAGATAAAAC	1800
Db	1741	AACTGTAGGCCCCCGAAACACAGCGGAGCTGTTTCTTCTTGA AAAACAGATAAAAC	1800
QY	1801	ATGGCGCCTATTAGGCTACTCTGCCAACAGACGCGAGCCTTACTTGGCTGATCATCTACT	1860
Db	1801	ATGGCGCCTATTAGGCTACTCTGCCAACAGACGCGAGCCTTACTTGGCTGATCATCTACT	1860
QY	1861	AGCCTCACAGCCGGGACAGAGAACCCAGTCTGAGAGGGAGAGTCTCAGTGTCTCCACC	1920
Db	1861	AGCCTCACAGCCGGGACAGAGAACCCAGTCTGAGAGGGAGAGTCTCAGTGTCTCCACC	1920
QY	1921	ACACATCTTTCCTGGCGACTCTGCTCAATGGCGTGTGTTGAGCTGTCTATCATGTGTCC	1980
Db	1921	ACACATCTTTCCTGGCGACTCTGCTCAATGGCGTGTGTTGAGCTGTCTATCATGTGTCC	1980
QY	1981	GGCTCAAGACCCCTTGGCGGCCCAAGAGGGGCCATCACCCTAATGTACACATGTGAC	2040
Db	1981	GGCTCAAGACCCCTTGGCGGCCCAAGAGGGGCCATCACCCTAATGTACACATGTGAC	2040
QY	2041	CAGAGCCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTACACATGACCTGTC	2100
Db	2041	CAGAGCCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTACACATGACCTGTC	2100
QY	2101	GGCAGCTCGGACCTTACTTGTGTACAGAGGACATGGCGATGTATTCGGTGGCGGGGG	2160
Db	2101	GGCAGCTCGGACCTTACTTGTGTGTACAGAGGACATGGCGATGTATTCGGTGGCGGGGG	2160
QY	2161	GGCGACAGCAGGGGAGCCTACTCTGCCAGCGCCGTCCTCTACTTGAAGGGCTTTGG	2220
Db	2161	GGCGACAGCAGGGGAGCCTACTCTGCCAGCGCCGTCCTCTACTTGAAGGGCTTTGG	2220
QY	2221	GGCGGTCCACTGCTCTGCCCCCTGGGGGACAGCTGTGGGATCTTTCGGGGCTCCGTTGC	2280
Db	2221	GGCGGTCCACTGCTCTGCCCCCTGGGGGACAGCTGTGGGATCTTTCGGGGCTCCGTTGC	2280
QY	2281	ACCCGAGGGGTTGGTGAAGGGCGGTGGATTTGTACCCGTCGAGTCTATGGAAACCTATG	2340
Db	2281	ACCCGAGGGGTTGGTGAAGGGCGGTGGATTTGTACCCGTCGAGTCTATGGAAACCTATG	2340
QY	2341	CGGTGCCCGGCTTCACGGACACATCGTCCCTCGGGCCGCTACCCGACATTCACAGTG	2400
Db	2341	CGGTGCCCGGCTTCACGGACACATCGTCCCTCGGGCCGCTACCCGACATTCACAGTG	2400
QY	2401	GCCCATCTACACGGCCCTACTGTGTAGGGGACAGACACTAAGGTGCGGCTGCTATGCA	2460
Db	2401	GCCCATCTACACGGCCCTACTGTGTAGGGGACAGACACTAAGGTGCGGCTGCTATGCA	2460
QY	2461	GCCCAAGGTTAAGGTGTGTGTCTGTCTGTACACCGCTCCGTCGGCCGACACCTAGGTTGCGG	2520
Db	2461	GCCCAAGGTTAAGGTGTGTGTCTGTGTGTACACCGCTCCGTCGGCCGACACCTAGGTTGCGG	2520
QY	2521	GGGTATGTGTAAAGGACATGTGTATGACACCTTACATCAGAACCGGGTAAAGGACATC	2580
Db	2521	GGGTATGTGTAAAGGACATGTGTATGACACCTTACATCAGAACCGGGTAAAGGACATC	2580
QY	2581	ACCCAGGGTGGCCCCATCAGTACTCCACTATGGCAAGTTTCTTCCGACAGGTGTTC	2640
Db	2581	ACCCAGGGTGGCCCCATCAGTACTCCACTATGGCAAGTTTCTTCCGACAGGTGTTC	2640
QY	2641	TCTGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCACTCACTCGACACT	2700
Db	2641	TCTGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCACTCACTCGACACT	2700
QY	2701	ATCTCGGGCATCGGCACAGTCTGTGGACCAAGCGGAGACAGCGCTGAGACGCTCGCTG	2760
Db	2701	ATCTCGGGCATCGGCACAGTCTGTGGACCAAGCGGAGACAGCGCTGAGACGCTCGCTG	2760
QY	2761	CTCGGCACCGCTAGCGCTCGGAGATCGGTACCGTGTGCACATCCAAACATCGAGGAGTG	2820
Db	2761	CTCGGCACCGCTAGCGCTCGGAGATCGGTACCGTGTGCACATCCAAACATCGAGGAGTG	2820

Db 4981 GGTGCTGAGAGTAGTGGAGGTTACGGGGTGGGGGATTTCCATACGTACAGGGGATG 5040
-QY 5041 ACCACTGACACGTAAAGTCCCGGTGAGGTTCCGGCCCCCGAATTCCTTCACAGAAATG 5100
Db 5042 ACCACTGACACGTAAAGTCCCGGTGAGGTTCCGGCCCCCGAATTCCTTCACAGAAATG 5100
QY 5101 GATGGGTCGGGTGACAGTAGCTCCAGGCTGCAAAACCCCTCTACGGAGAGAGTGC 5160
Db 5101 GATGGGTCGGGTGACAGTAGCTCCAGGCTGCAAAACCCCTCTACGGAGAGAGTGC 5160
QY 5161 ACATTCCTGGTGGGCTCATCATCAATCACTGTTGGGTGACAGCTCCCATGCGAACCCGAA 5220
Db 5161 ACATTCCTGGTGGGCTCATCATCAATCACTGTTGGGTGACAGCTCCCATGCGAACCCGAA 5220
QY 5221 CCGAGCTAGCACTGCTCCTCCATGCTCACCGAGCCCTCCCATATACGGCGGAGACG 5280
Db 5221 CCGAGCTAGCACTGCTCCTCCATGCTCACCGAGCCCTCCCATATACGGCGGAGACG 5280
QY 5281 GCTAAGCTAGGCTGGCCAGGGGATCTCCCTCCCTTGGCCAGCTCATCAGCTAGCCAG 5340
Db 5281 GCTAAGCTAGGCTGGCCAGGGGATCTCCCTCCCTTGGCCAGCTCATCAGCTAGCCAG 5340
QY 5341 CTGTGCGGCTTCTCTGAGGCAACATGCACTACCCGTCAATGACTCCCGGAGCTGAC 5400
Db 5341 CTGTGCGGCTTCTCTGAGGCAACATGCACTACCCGTCAATGACTCCCGGAGCTGAC 5400
QY 5401 CTCATGAGGCCAACCTCTGTGGGGAGAGATGGCGGGAACATCACCCGCTGGAG 5460
Db 5401 CTCATGAGGCCAACCTCTGTGGGGAGAGATGGCGGGAACATCACCCGCTGGAG 5460
QY 5461 TCAGAAATAAGTAGTAATTTTGGACTTTTCAGCCGCTCCAGCCGAGAGAGATGAG 5520
Db 5461 TCAGAAATAAGTAGTAATTTTGGACTTTTCAGCCGCTCCAGCCGAGAGATGAG 5520
QY 5521 AAGGAGTAGTCCGCTCCGGGAGATCTCGGAGGTCAGAGAAATTCCTCGAGAGTATG 5580
Db 5521 AAGGAGTAGTCCGCTCCGGGAGATCTCGGAGGTCAGAGAAATTCCTCGAGAGTATG 5580
QY 5581 CCCATATGGGACGCCCGGATTAACACCTCCACTGTAGTAGTCTCGAGAGAGAGCCGAG 5640
Db 5581 CCCATATGGGACGCCCGGATTAACACCTCCACTGTAGTAGTCTCGAGAGAGAGCCGAG 5640
QY 5641 TAGTCCCTCAAGTGTACAGGAGTGTCCATGCGGCTCGCAAGGCCCTCCCATACCA 5700
Db 5641 TAGTCCCTCAAGTGTACAGGAGTGTCCATGCGGCTCGCAAGGCCCTCCCATACCA 5700
QY 5701 CCTCAAGGAGAGAGAGAGTGTCTGCTGTCAGATCTACCGTGTCTTGGCTTGGCG 5760
Db 5701 CCTCAAGGAGAGAGAGAGTGTCTGCTGTCAGATCTACCGTGTCTTGGCTTGGCG 5760
QY 5761 GAGCTGGCCACAAGACCTTGGGACGCTCCGATGCTGAGATCTACCGTGTCTTGGCG 5820
Db 5761 GAGCTGGCCACAAGACCTTGGGACGCTCCGATGCTGAGATCTACCGTGTCTTGGCG 5820
QY 5821 ACGGCTCTCTGACAGCCCTTCGACGACGCGGAGCTCGAGCTTGGAGTGGAC 5880
Db 5821 ACGGCTCTCTGACAGCCCTTCGACGACGCGGAGCTCGAGCTTGGAGTGGAC 5880
QY 5881 TCCCTCATGCCCCCTTAGGGGGAGGCCGGGGATCCCGATCTCAGGAGAGGGTCTTGG 5940
Db 5881 TCCCTCATGCCCCCTTAGGGGGAGGCCGGGGATCCCGATCTCAGGAGAGGGTCTTGG 5940
QY 5941 TCTACCGTAAGGAGAGGCTAGTGAGAGCTGCTGCTGCTGATGCTTCTACACATGG 6000
Db 5941 TCTACCGTAAGGAGAGGCTAGTGAGAGCTGCTGCTGCTGATGCTTCTACACATGG 6000
QY 6001 ACGAGGCGCTGATCAGCGCATGCGCTGGGAGGAAACAGAGTCCCATTAATGCACTG 6060
Db 6001 ACGAGGCGCTGATCAGCGCATGCGCTGGGAGGAAACAGAGTCCCATTAATGCACTG 6060
QY 6061 AGCAACTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6120
Db 6061 AGCAACTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6120

QY 6121 CTGGGCGACAGAGAGTCACTTTGACAGACTCCAGGCTCTGGAGACACTACCGGGAC 6180
Db 6121 CTGGGCGACAGAGAGTCACTTTGACAGACTCCAGGCTCTGGAGACACTACCGGGAC 6180
QY 6181 GTGCTCAAGAGATGAAGCGGAGGCTCCAGTGAAGGCTTAACCTCTATCCGTGGAG 6240
Db 6181 GTGCTCAAGAGATGAAGCGGAGGCTCCAGTGAAGGCTTAACCTCTATCCGTGGAG 6240
QY 6241 GAAAGCTTAAGCTGACGCCCCACATTTGGGCGAGATCTAAATTTGGCTATGGGCAAG 6300
Db 6241 GAAAGCTTAAGCTGACGCCCCACATTTGGGCGAGATCTAAATTTGGCTATGGGCAAG 6300
QY 6301 GAGGCTCGGAGCTTCCGAGAGGCGGTAAACCATCATCGCTCCGTTGGAAGAGCTTG 6360
Db 6301 GAGGCTCGGAGCTTCCGAGAGGCGGTAAACCATCATCGCTCCGTTGGAAGAGCTTG 6360
QY 6361 CTGGAAGACACTGAGACACCAATTGACACACCATCATGGAACCAAAATGAGGTTTCTGC 6420
Db 6361 CTGGAAGACACTGAGACACCAATTGACACACCATCATGGAACCAAAATGAGGTTTCTGC 6420
QY 6421 GTCCAAACAGAGAGGGGGCGGCAAGCAGTCCCTATCTGATTCGAGATTGGGG 6480
Db 6421 GTCCAAACAGAGAGGGGGCGGCAAGCAGTCCCTATCTGATTCGAGATTGGGG 6480
QY 6481 GTTCGTGTGTGAGAGAAATGGCCCTTACGATGTGTCTCCACCCCTCCAGGCGTG 6540
Db 6481 GTTCGTGTGTGAGAGAAATGGCCCTTACGATGTGTCTCCACCCCTCCAGGCGTG 6540
QY 6541 ATGGGCTCTTCAATAGGATTCATATCTCTCTGAGAGCGGGGTGAGTTCTCTGTAAT 6600
Db 6541 ATGGGCTCTTCAATAGGATTCATATCTCTCTGAGAGCGGGGTGAGTTCTCTGTAAT 6600
QY 6601 GCCTGGAAGCGAAGAAATGGCTTATGGGCTTTCGATATGACACCCGCTGTTTGACTCA 6660
Db 6601 GCCTGGAAGCGAAGAAATGGCTTATGGGCTTTCGATATGACACCCGCTGTTTGACTCA 6660
QY 6661 ACGGTACTGAGAAATGACATCCGTGTGAGAGATTAATCTACCAATGTTGACTTGGCC 6720
Db 6661 ACGGTACTGAGAAATGACATCCGTGTGAGAGATTAATCTACCAATGTTGACTTGGCC 6720
QY 6721 CCCGAGCCAGACAGGCGCATTAAGGTCGCTCAGAGAGCGGCTTACATGGGAGGCGCCCTG 6780
Db 6721 CCCGAGCCAGACAGGCGCATTAAGGTCGCTCAGAGAGCGGCTTACATGGGAGGCGCCCTG 6780
QY 6781 ACTAATTCCTAAAGGCGAGACTGCGGCTATGCGGCTCCGCGAGCGGTGTACTGACG 6840
Db 6781 ACTAATTCCTAAAGGCGAGACTGCGGCTATGCGGCTCCGCGAGCGGTGTACTGACG 6840
QY 6841 ACCAGCTGGGTAATACCTTCATGTTACTGGAAGCGGCTGCGGCTGTCGAGCTGGC 6900
Db 6841 ACCAGCTGGGTAATACCTTCATGTTACTGGAAGCGGCTGCGGCTGTCGAGCTGGC 6900
QY 6901 AAGCTTCAGAGCTGACAGTGTCTGTATGCGGAGACGCTTGTGCTTATCTGGAAGC 6960
Db 6901 AAGCTTCAGAGCTGACAGTGTCTGTATGCGGAGACGCTTGTGCTTATCTGGAAGC 6960
QY 6961 GCGGGAGCCCAAGAGAGAGGCGAGGCTTACGAGGCTTCAAGGAGGCTATCAAGATAC 7020
Db 6961 GCGGGAGCCCAAGAGAGAGGCGAGGCTTACGAGGCTTCAAGGAGGCTATCAAGATAC 7020
QY 7021 TCTGCCCCCTCGGGGAGCCCGCCCAACAGATACGACTTGGAGTTGATTAACATCATGC 7080
Db 7021 TCTGCCCCCTCGGGGAGCCCGCCCAACAGATACGACTTGGAGTTGATTAACATCATGC 7080
QY 7081 TCTTCAATGTGTAGTGGCGGAGTGCATGCTGCGCAAAAGGCTATCTATCTACCCGT 7140
Db 7081 TCTTCAATGTGTAGTGGCGGAGTGCATGCTGCGCAAAAGGCTATCTATCTACCCGT 7140
QY 7141 GACCCACACACCCCTTGGCGGCGCTGCTGCGAGAGCTAGACACACTCTCAGTCAAT 7200
Db 7141 GACCCACACACCCCTTGGCGGCGCTGCTGCGAGAGAGTATAGACACACTCTCAGTCAAT 7200

QY 7201 TCCTGCTAGGACATCATCATGTATGAGGCCACCTTGTGGGACAGATGATCTGTATG 7260
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Db 7201 TCGTGGCTAGGACATCATCATGTATGAGGCCACCTTGTGGGACAGATGATCTGTATG 7260
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QY 7261 ACTCATTTCTTCATCTCTTCTAGCTCAGGAACAACCTTGAAAAAGCCCTAGATTGTGAG 7320
|||||
Db 7261 ACTCATTTCTTCATCTCTTCTAGCTCAGGAACAACCTTGAAAAAGCCCTAGATTGTGAG 7320
|||||
QY 7321 ATCTAGGGGCGCTTCTCATTTGAGCCACTGACCTACCTACATTCATTCAGAGACTC 7380
|||||
Db 7321 ATCTAGGGGCGCTTCTCATTTGAGCCACTGACCTACCTACATTCATTCAGAGACTC 7380
|||||
QY 7381 CATGCGCTTAGCGCATTTTCTCATAGTAGTACTCTCCAGGTGAGATCAATAGGGTGCT 7440
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Db 7381 CATGCGCTTAGCGCATTTTCTCATAGTAGTACTCTCCAGGTGAGATCAATAGGGTGCT 7440
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QY 7441 TCATGCTCAGGAACCTTGGGGTACCGCCCTTGCGAGTGTGGAGACATGSGCCAGAAAT 7500
|||||
Db 7441 TCATGCTCAGGAACCTTGGGGTACCGCCCTTGCGAGTGTGGAGACATGSGCCAGAAAT 7500
|||||
QY 7501 GTCCGCGCTTAGGCTACTGTCCAGGGGGAGGGGTGCGACATTGTGGCAATGACTCTTC 7560
|||||
Db 7501 GTCCGCGCTTAGGCTACTGTCCAGGGGGAGGGGTGCGACATTGTGGCAATGACTCTTC 7560
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QY 7561 AACTGGGCGATGAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGCCAGTTGGAT 7620
|||||
Db 7561 AACTGGGCGATGAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGCCAGTTGGAT 7620
|||||
QY 7621 TTATCAGAGCTGTGCTGTGTCTTACAGCGGGGAGACATATATCACAGCTGTCTGCT 7680
|||||
Db 7621 TTATCAGAGCTGTGCTGTGTCTTACAGCGGGGAGACATATATCACAGCTGTCTGCT 7680
|||||
QY 7681 GCCGAGCCCGCTGTGCTCATGTGTGCTACTCTTCTGTAGGGGTAGGCAATCAT 7740
|||||
Db 7681 GCCGAGCCCGCTGTGCTCATGTGTGCTACTCTTCTGTAGGGGTAGGCAATCAT 7740
|||||
QY 7741 CTACTCCCAACCGATGAGAGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTT 7800
|||||
Db 7741 CTACTCCCAACCGATGAGAGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTT 7800
|||||
QY 7801 TTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
|||||
Db 7801 TTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
|||||
QY 7861 TTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
|||||
Db 7861 TTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
|||||
QY 7921 TAGCTGGAAGGTCCTGTGAGCGCTGAGACTGAGAGAGTGTGATCTGGCTCTCTGC 7980
|||||
Db 7921 TAGCTGGAAGGTCCTGTGAGCGCTGAGACTGAGAGAGTGTGATCTGGCTCTCTGC 7980
|||||
QY 7981 AGATCAAGTACT 7992
|||||
Db 7981 AGATCAAGTACT 7992
|||||

RESULT 7
AAL47279
ID AAL47279 standard; DNA: 7991 BP.

XX 30-AUG-2002 (first entry)
DE Hepatitis C virus sub-genomic replicon recombinant clone HCV9.
XX
KW Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
XX
OS viroide; hepatotropic; gene therapy; anti-viral; gene; ds.
XX
PN Hepatitis C virus.
PN WO200238793-A2.

XX
PD 16-MAY-2002.
XX
PF 02-NOV-2001; 2001MO-US46350.
XX
PR 07-NOV-2000; 2000US-245866P.
XX
PA (ANAD-) ANADYS PHARM INC.
XX
PI Bichko V.
XX
DR WPI: 2002-49082/52.
PT Novel nucleic acid encoding replication competent recombinant hepatitis
PT C virus genome useful for screening anti-hepatitis C virus therapeutics
PT and for vaccine development
XX
PS Claim 9: Page 61-65; 85pp; English.
CC The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement
CC non-infectious, replication-defective infection-component, and
CC replication-defective non-infectious HCV. In gene therapy or gene
CC vaccination targeted to hepatic tissue for treating an animal infected or
CC susceptible to HCV infection and for studying HCV infection and
CC propagation. The present sequence is a clone of a fragment of the HCV
CC genome designated HCV9.
XX
SQ Sequence 7991 BP; 1647 A; 2369 C; 2245 G; 1730 T; 0 other;
Query Match 99.8%; Score 7980; DB 24; Length 7991;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCCAGCCCCGATTTGGGGGGGACACTCCACATAGATCACTCCCTGGAGGAACTACTG 60
Db 1 GCCAGCCCCGATTTGGGGGGGACACTCCACATAGATCACTCCCTGGAGGAACTACTG 60
QY 61 TCTTACGAGAAAGCGCTAGCCATGGCGTTAGTATGAGTGTGTGACGCTCCAGGAC 120
Db 61 TCTTACGAGAAAGCGCTAGCCATGGCGTTAGTATGAGTGTGTGACGCTCCAGGAC 120
QY 121 CCCCCCTCCGGGAGAGCCATAGTGTGCGGAAACGGGTGAGTACCGGAAATGGCAG 180
Db 121 CCCCCCTCCGGGAGAGCCATAGTGTGCGGAAACGGGTGAGTACCGGAAATGGCAG 180
QY 181 GACGACCGGGTCTTTCTTGATCAACCGCTCAATGCTGTGAGATTGGCGGTGCCCC 240
Db 181 GACGACCGGGTCTTTCTTGATCAACCGCTCAATGCTGTGAGATTGGCGGTGCCCC 240
QY 241 GCGAGATGCTAGCCGAGTGTGTGTGCGGAAAGGCTGTGTAGTGTCTATAGG 300
Db 241 GCGAGATGCTAGCCGAGTGTGTGTGCGGAAAGGCTGTGTAGTGTCTATAGG 300
QY 301 GTGCTTGCAGTCCCGGAGGAGTCTGAGACCGTGCACATGAGACAGAAATCTTAAC 360
Db 301 GTGCTTGCAGTCCCGGAGGAGTCTGAGACCGTGCACATGAGACAGAAATCTTAAC 360
QY 361 CTCAAGAAAAACCAAGGCGGCGCATGTTGAAACAAATGATTGCGAGAGTTCTC 420
Db 361 CTCAAGAAAAACCAAGGCGGCGCATGATTGAAACAAATGATTGCGAGAGTTCTC 420
QY 421 CGGCGGCTTGGTGGAGAGGCTATTGCTATGACTGCGCACAAAGACAAATCGGCTCT 480
Db 421 CGGCGGCTTGGTGGAGAGGCTATTGCTATGACTGCGCACAAAGACAAATCGGCTCT 480
QY 481 CTGATGCCGCCGTTCGCGCTGTACGCGAGGGGCGCCGGTCTTTTGTCAAGACCG 540

QY 2701 ATCTGGGATGGGACAGTCTCTGGACCAAGCGAGCGGTGAGCGGACTGCTGCTG 2760
|||||
Db 2700 ATCTGGGATGGGACAGTCTCTGGACCAAGCGAGCGGTGAGCGGACTGCTGCTG 2759
QY 2761 CTCGCCACGCTACGCTCCGGGATGCGTACACGTGCCACATCCAAACATCGAGAGTG 2820
|||||
Db 2760 CTCGCCACGCTACGCTCCGGGATGCGTACACGTGCCACATCCAAACATCGAGAGTG 2819
QY 2821 GCTCTGCCAGACGTGAGAAATCCCTTTTATGCAAGCCATCCCATGAGACATC 2880
|||||
Db 2820 GCTCTGCCAGACGTGAGAAATCCCTTTTATGCAAGCCATCCCATGAGACATC 2879
QY 2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCCAGAAATGTGATGACCTGCGCG 2940
|||||
Db 2880 AAGGGGGGAGGACCTCATTTTCTGCCATTCCAGAAATGTGATGACCTGCGCG 2939
QY 2941 AAGCTGCGGGCTGGGACTCATGCTGATGATATTAACGGGGCTTGATGTACGTC 3000
|||||
Db 2940 AAGCTGCGGGCTGGGACTCATGCTGATGATATTAACGGGGCTTGATGTACGTC 2999
QY 3001 ATACCACTAGCGGAGACGTCTATGTCGAGCAAGGACGCTCTAATGACGGCTTTAC 3060
|||||
Db 3000 ATACCACTAGCGGAGACGTCTATGTCGAGCAAGGACGCTCTAATGACGGCTTTAC 3059
QY 3061 GGGGATTTGACACGTGATGACATGATGTCACCCAGACAGTGCATTCAGC 3120
|||||
Db 3060 GGGGATTTGACACGTGATGACATGATGTCACCCAGACAGTGCATTCAGC 3119
QY 3121 CTCGACCCGACCTTCACATTTGAGAGGACGCGTCCCAAGACGGGTGTACGCTCG 3180
|||||
Db 3120 CTCGACCCGACCTTCACATTTGAGAGGACGCGTCCCAAGACGGGTGTACGCTCG 3179
QY 3181 CACCGGAGGACGAGCTGATGAGGGGAGGATGGGATTTGATGATCCAGGA 3240
|||||
Db 3180 CACCGGAGGACGAGCTGATGAGGGGAGGATGGGATTTGATGATCCAGGA 3239
QY 3241 GAAGGGCCCTCGGGCATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
|||||
Db 3240 GAAGGGCCCTCGGGCATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3299
QY 3301 GCTTGGTACGAGCTACGCGCCCGGAGACCTCATGATGCTGCGGGCTTAACTAACCA 3360
|||||
Db 3300 GCTTGGTACGAGCTACGCGCCCGGAGACCTCATGATGCTGCGGGCTTAACTAACCA 3359
QY 3361 CCAGGGTTCCTGCTGCCAGGACCATGAGATTCTGGAGAGCGTCTTTACAGGCTTC 3420
|||||
Db 3360 CCAGGGTTCCTGCTGCCAGGACCATGAGATTCTGGAGAGCGTCTTTACAGGCTTC 3419
QY 3421 ACCACATAGACGCCCTTTCTGCTGCCAGACTAACGAGGACAGAACTTCCCTTAC 3480
|||||
Db 3420 ACCACATAGACGCCCTTTCTGCTGCCAGACTAACGAGGACAGAACTTCCCTTAC 3479
QY 3481 CTGTAGCATACGAGGTGAGGTGCGCCAGGGCTCAGGCTCCACCTCATGCTGAGAC 3540
|||||
Db 3480 CTGTAGCATACGAGGTGAGGTGCGCCAGGGCTCAGGCTCCACCTCATGCTGAGAC 3539
QY 3541 CAATGTGGAAGTGTCTCATAGGCTTAAGCCTACGCTGACAGGGCCAAAGCCCTGCTG 3600
|||||
Db 3540 CAATGTGGAAGTGTCTCATAGGCTTAAGCCTACGCTGACAGGGCCAAAGCCCTGCTG 3599
QY 3601 TATAGGCTGGAGGCGCTTCAAAAGGAGGTACTACACACACCCCTTAACCAATACATC 3660
|||||
Db 3600 TATAGGCTGGAGGCGCTTCAAAAGGAGGTACTACACACACCCCTTAACCAATACATC 3659
QY 3661 ATGCGATGCAATGCGCTGACCTGAGAGTGTGACAGACCTGAGTGTGATGAGCGGA 3720
|||||
Db 3660 ATGCGATGCAATGCGCTGACCTGAGAGTGTGACAGACCTGAGTGTGATGAGCGGA 3719
QY 3721 GTCTAGAGAGCTGCGCGGCTATGCTGACAAAGGAGCGGTGCTCACTTGGGGCAGG 3780
|||||
Db 3720 GTCTAGAGAGCTGCGCGGCTATGCTGACAAAGGAGCGGTGCTCACTTGGGGCAGG 3779

QY 3781 ATCATCTTGTCCGGAAGCGCCGCAATCTCCGACAGGGAAGTCTTTACCGGGAGTTC 3840
|||||
Db 3780 ATCATCTTGTCCGGAAGCGCCGCAATCTCCGACAGGGAAGTCTTTACCGGGAGTTC 3839
QY 3841 GATGATGAGAGTGGGCTCACAGCTTCCCTTACATCGAAGAGGGAATGACACTGCGC 3900
|||||
Db 3840 GATGATGAGAGTGGGCTCACAGCTTCCCTTACATCGAAGAGGGAATGACACTGCGC 3899
QY 3901 GAACAATTCAAACAGAGGCAATCGGTTGCTGCAAAAGCAGCCCAAGCAAGCGGAGCT 3960
|||||
Db 3900 GAACAATTCAAACAGAGGCAATCGGTTGCTGCAAAAGCAGCCCAAGCAAGCGGAGCT 3959
QY 3961 GCTGCTCCCGTGTGGAATCCAGTGGGAGCCCTCGAAGCCCTCTGGGGCAACATATG 4020
|||||
Db 3960 GCTGCTCCCGTGTGGAATCCAGTGGGAGCCCTCGAAGCCCTCTGGGGCAACATATG 4019
QY 4021 TGAATTTTCATACGCGGGATACATATTTTACAGAGCTTGTCACTGTGCTGCAACCCC 4080
|||||
Db 4020 TGAATTTTCATACGCGGGATACATATTTTACAGAGCTTGTCACTGTGCTGCAACCCC 4079
QY 4081 GCGATGACATCACTGATGAGCTTCAACAGCTCTATCAACAGCCGCTCACCAACCAT 4140
|||||
Db 4080 GCGATGACATCACTGATGAGCTTCAACAGCTCTATCAACAGCCGCTCACCAACCAT 4139
QY 4141 ACCCTCTGTTCATCTCTGGGGGATGGGTGGCCGCGCAACTTGTCTCTCCAGCGCT 4200
|||||
Db 4140 ACCCTCTGTTCATCTCTGGGGGATGGGTGGCCGCGCAACTTGTCTCTCCAGCGCT 4199
QY 4201 GCTTGTGCTTTGTAGGCGCCGCGCATCGTGGAGCGGCTGTTGGCAGATATGGCTTGG 4260
|||||
Db 4200 GCTTGTGCTTTGTAGGCGCCGCGCATCGTGGAGCGGCTGTTGGCAGATATGGCTTGG 4259
QY 4261 AAGTCTGTGGATATTTTGGCAGGTTATGAGCAGGGGTATGAGCGCGCTGTGCGCC 4320
|||||
Db 4260 AAGTCTGTGGATATTTTGGCAGGTTATGAGCAGGGGTATGAGCGCGCTGTGCGCC 4319
QY 4321 TTTAAGTCAATGAGCGGCGAGATGCCCTCACCGAGACCTGAGCTAACCTACTCCCTGCT 4380
|||||
Db 4320 TTTAAGTCAATGAGCGGCGAGATGCCCTCACCGAGAGCTGAGCTAACCTACTCCCTGCT 4379
QY 4381 ATCCTCTCCCTGGCGCCTAGTCTGCGGGGCTGCTGCTGCGAGCAGTACTGCTGCGCAC 4440
|||||
Db 4380 ATCCTCTCCCTGGCGCCTAGTCTGCGGGGCTGCTGCTGCGAGCAGTACTGCTGCGCAC 4439
QY 4441 GTGGGCCAGGGGAGGGGCTGTGCACTGATGATGAACCGGCTATAGCTTGTGCTTCGCG 4500
|||||
Db 4440 GTGGGCCAGGGGAGGGGCTGTGCACTGATGATGAACCGGCTATAGCTTGTGCTTCGCG 4499
QY 4501 GGTACACAGTCTCCGCCACGCACTATGCTGAGAGGAGCGTGCAGCAGCTGTCACT 4560
|||||
Db 4500 GGTACACAGTCTCCGCCACGCACTATGCTGAGAGGAGCGTGCAGCAGCTGTCACT 4559
QY 4561 CAGATCTCTCTAGCTTTACACTACCTACGCTGTAAGAGGCTTCACAGTGAATCAAC 4620
|||||
Db 4560 CAGATCTCTCTAGCTTTACACTACCTACGCTGTAAGAGGCTTCACAGTGAATCAAC 4619
QY 4621 GAGGACTGCTCAAGGCGATGCTCGGCTGCTGAGCTTAAGATGTTGGATGATGATGAC 4680
|||||
Db 4620 GAGGACTGCTCAAGGCGATGCTCGGCTGCTGAGCTTAAGATGTTGGATGATGATGAC 4679
QY 4681 ACGGTGTGAGATGATTTCAAGACCTGGCTCAAGTCCAGCTCTGCCGATGTGCGGGA 4740
|||||
Db 4680 ACGGTGTGAGATGATTTCAAGACCTGGCTCAAGTCCAGCTCTGCCGATGTGCGGGA 4739
QY 4741 GTCCCTCTCTCTCATGCTCAAGCTGGGTCAAGGAGGTGTGGCGGGGCGAGGCTCATG 4800
|||||
Db 4740 GTCCCTCTCTCTCATGCTCAAGCTGGGTCAAGGAGGTGTGGCGGGGCGAGGCTCATG 4799
QY 4801 CAACACACCTGCGCATGTGAGCAGATCACCGGACATGTAAAAAAGATTCATGAGG 4860
|||||
Db 4800 CAACACACCTGCGCATGTGAGCAGATCACCGGACATGTAAAAAAGATTCATGAGG 4859
QY 4861 ATGCTGGGGCTTAGAGCTGTAGTAAACAGTGGCAATGAAACATTTCCCCATTAACCGGTAC 4920

|||||
Db 4860 ATGTGGGGCTTAGACCTGTAGTAAACGCTGCATGGAACATTTCCCATTAACGGGTAC 4919
QY 4921 ACCAAGGGCCCCCTGCACAGCCCTCCCGGGCCCAATATATCTAGGGCGCTGTGGGGTG 4980
Db 4920 ACCAAGGGCCCCCTGCACAGCCCTCCCGGGCCCAATATATCTAGGGCGCTGTGGGGTG 4979
QY 4981 GCTGCTGAGAGTACGTGAGGTTACCGGGGTGGGGATTCCACTACGTGACGGGATG 5040
Db 4980 GCTGCTGAGAGTACGTGAGGTTACCGGGGTGGGGATTCCACTACGTGACGGGATG 5039
QY 5041 ACCACTGACAACGTAAAGTGGCCGTGTCAGTTCGGGCCCGGATTTCTTCACAGAGTG 5100
Db 5040 ACCACTGACAACGTAAAGTGGCCGTGTCAGTTCGGGCCCGGATTTCTTCACAGAGTG 5099
QY 5101 GATGGGGTGGGGTTGCACAGGTACGTCACGCGTGCACAAACCCCTCCTACGGGAGAGTGC 5160
Db 5100 GATGGGGTGGGGTTGCACAGGTACGTCACGCGTGCACAAACCCCTCCTACGGGAGAGTGC 5159
QY 5161 ACATTCTGTCGGGCTCAATCAATACCTGTTGGGTTCACAGTCCCATGCGAGCCGGA 5220
Db 5160 ACATTCTGTCGGGCTCAATCAATACCTGTTGGGTTCACAGTCCCATGCGAGCCGGA 5219
QY 5221 CCGGACGTAGACGTGCTCACTTCATGCTCACCGACCCCTCCACATTACGGCGAGAGC 5280
Db 5220 CCGGACGTAGACGTGCTCACTTCATGCTCACCGACCCCTCCACATTACGGCGAGAGC 5279
QY 5281 GCTAGAGTGGGTGGGCGACGGGATGTCCTCCCTCCTTGGCCAGCTCATACCTAGCCAG 5340
Db 5280 GCTAGAGTGGGTGGGCGACGGGATGTCCTCCCTCCTTGGCCAGCTCATACCTAGCCAG 5339
QY 5341 CTGTCTGGGCTTCCTTGAAGGACACATGCACTACCCGTCATGACTCCCGGACGCTGAC 5400
Db 5340 CTGTCTGGGCTTCCTTGAAGGACACATGCACTACCCGTCATGACTCCCGGACGCTGAC 5399
QY 5401 CTCAATGAGGCCAACCTCCTGTGGCGGACAGATGGCGGGGAACATCCCGCTGAG 5460
Db 5400 CTCAATGAGGCCAACCTCCTGTGGCGGACAGATGGCGGGGAACATCCCGCTGAG 5459
QY 5461 TCAGAAATAGAGTAGTAAATTTTGAAGTCTTTCGAGCCGCTCCAAACGAGAGAGTAG 5520
Db 5460 TCAGAAATAGAGTAGTAAATTTTGAAGTCTTTCGAGCCGCTCCAAACGAGAGAGTAG 5519
QY 5521 AGGAAATATCCGTTCCGGGGAGATCTTCGAGAGTCCAGAAATTTCCCTGAGCCATG 5580
Db 5520 AGGAAATATCCGTTCCGGGGAGATCTTCGAGAGTCCAGAAATTTCCCTGAGCCATG 5579
QY 5581 CCCATATGGGACGCGCCGAGTTACAAACCTCCACTGTAGAGTCTCGAAGAACCCGGAC 5640
Db 5580 CCCATATGGGACGCGCCGAGTTACAAACCTCCACTGTAGAGTCTCGAAGAACCCGGAC 5639
QY 5641 TAGTCCTTCCAGTGTACACGGGGTTCATTGCGCGCTGCCAAGGCCCTCCGATACCA 5700
Db 5640 TAGTCCTTCCAGTGTACACGGGGTTCATTGCGCGCTGCCAAGGCCCTCCGATACCA 5699
QY 5701 CCTCCAGGAGAGAGAGAGAGTGTGCTGCTAGAAATCAACGCTGCTTCGCTTGGCG 5760
Db 5700 CCTCCAGGAGAGAGAGAGAGTGTGCTGCTAGAAATCAACGCTGCTTCGCTTGGCG 5759
QY 5761 GAGCTGCGCAAAAGACCTTGGCAGCTCCGAATCGTCGCGCGTGCAGACGCGACGCA 5820
Db 5760 GAGCTGCGCAAAAGACCTTGGCAGCTCCGAATCGTCGCGCGTGCAGACGCGACGCA 5819
QY 5821 ACCGCTCTGCTGACGAGCCCTCCGACGAGCGAGCGGAGTCCGAGCTGAGTCGAC 5880
Db 5820 ACCGCTCTGCTGACGAGCCCTCCGACGAGCGGAGTCCGAGCTGAGTCGAC 5879
QY 5881 TCTCTCATGCCCCCTTGAAGGGGAGCGGGGATCCCGATCTCAGCGACGGGTCTTGG 5940
Db 5880 TCTCTCATGCCCCCTTGAAGGGGAGCGGGGATCCCGATCTCAGCGACGGGTCTTGG 5939
QY 5941 TCTACCTTAGCGAGAGGTAGTAGAGAGTCTGCTGCTCATGTCTTACCATG 6000
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Db 5940 TCTACCTTAGCGAGAGGTAGTAGAGAGTCTGCTGCTGCTCATGTCTTACCATG 5999
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Db 6000 ACAGAGGCCCTGATCAGCCATGCGGTGGGAGAGAAACCAAGTGGCCATCATATGACTG 6059
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Db 6060 AGCACTCTTTGCTCGCTACCAACAACTTGCTATGCTTACCAACATCTGCAGCGCAAC 6119
QY 6121 CTGGCGGAGAAAGGTCACCTTTCAGAGCTGACGCTCGTGGAGACCACTACCGGAC 6180
Db 6120 CTGGCGGAGAAAGGTCACCTTTCAGAGCTGACGCTCGTGGAGACCACTACCGGAC 6179
QY 6181 GTGCTCAAGAGATGAAGGGGAGGCGTCCACAGTTAAGGCTTAACTTATCCGTGAG 6240
Db 6180 GTGCTCAAGAGATGAAGGGGAGGCGTCCACAGTTAAGGCTTAACTTATCCGTGAG 6239
QY 6241 GAAGCTCTTAAGTGAAGCCCCCACAATTGGCGAGATCTAAATTTGGCTATGGGCAAG 6300
Db 6240 GAAGCTCTTAAGTGAAGCCCCCACAATTGGCGAGATCTAAATTTGGCTATGGGCAAG 6299
QY 6301 GACGTCCGGAACCTATCCAGAGCCGTTAACCATCCGCTCGTGGAGAGACTTG 6360
Db 6300 GACGTCCGGAACCTATCCAGAGCCGTTAACCATCCGCTCGTGGAGAGACTTG 6359
QY 6361 CTGGAACACACTGAGACACCAATTGACACCACCATATGAGCAAAAATAGAGTTTCTGC 6420
Db 6360 CTGGAACACACTGAGACACCAATTGACACCACCATATGAGCAAAAATAGAGTTTCTGC 6419
QY 6421 GTCCAAACAGAGAGGGGGCCGCAAGCCAGCTGCGCTTATGCTATCCCATATTGGG 6480
Db 6420 GTCCAAACAGAGAGGGGGCCGCAAGCCAGCTGCGCTTATGCTATCCCATATTGGG 6479
QY 6481 GTTCGTGTGCGAGAAATGSCCTTTACAGATGTGTCTCAACCTCCCTAGGCCGTG 6540
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QY 6541 ATGGGCTCTTCATACGATTCCAATCTCTCTGGAGACGCGGTGAGTTCCTGGTGAAT 6600
Db 6540 ATGGGCTCTTCATACGATTCCAATCTCTCTGGAGACGCGGTGAGTTCCTGGTGAAT 6599
QY 6601 GCTGGAAGCGAAGAAATGCCCTTTACAGATGTGTCTCAACCTCCCTAGGCCGTG 6660
Db 6600 GCTGGAAGCGAAGAAATGCCCTTTACAGATGTGTCTCAACCTCCCTAGGCCGTG 6659
QY 6661 ACGGTCTAGATGATGATCGGTGTTGAGAGTCAATACCAATGTTGACTTGGCC 6720
Db 6660 ACGGTCTAGATGATGATCGGTGTTGAGAGTCAATACCAATGTTGACTTGGCC 6719
QY 6721 CCGGAACCGACAGGCGCATTAAGTGCCTACAGACGCGCTTTAATGCGGGGCCCTTG 6780
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QY 6781 ACTAATCTTAAAGGAGAACTCGGCTTCGCGCGTGGCGGAGCGGTTACTGACG 6840
Db 6780 ACTAATCTTAAAGGAGAACTCGGCTTCGCGCGTGGCGGAGCGGTTACTGACG 6839
QY 6841 ACCAGCTGCGGTATACCTTCACATGTTACTTGAAGGCGGTGCGGCGTGGAGCTCG 6900
Db 6840 ACCAGCTGCGGTATACCTTCACATGTTACTTGAAGGCGGTGCGGCGTGGAGCTCG 6899
QY 6901 AAGCTCAGAGCTGACGATGCTCTGATGCGGAGACGACTTGTGTTATCTGTAAGG 6960
Db 6900 AAGCTCAGAGCTGACGATGCTCTGATGCGGAGACGACTTGTGTTATCTGTAAGG 6959
QY 6961 GCGGGGACCAAGAGACAGAGGAGCTACGAGGCTTCACGAGAGCTATGACTGATAC 7020
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QY 7021 TCTGCCCCCTTGGGAGCCGCCCAACCAAGATACGACTTGGAGTTGATAACATCATGC 7080
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DB 7080 TCCTCCAAATGTGTCACTGCGGCGACGATGCATCTGGCAAAAGGGTGTACTATCTCACCCGT 7139
OY 7141 GACCCACACACCCCGCTTCCGGGGGTGGTGGGAGAGAGGTAGACACACCCAGTCAAT 7200
DB 7140 GACCCACACACCCCGCTTCCGGGGGTGGTGGGAGAGAGGTAGACACACCCAGTCAAT 7199
OY 7201 TCCTGGCTAGGCAACATCATCATGTATGGGCCACCTTGTGGGCAAGGATGATCCTGATG 7260
DB 7200 TCCTGGCTAGGCAACATCATCATGTATGGGCCACCTTGTGGGCAAGGATGATCCTGATG 7259
OY 7261 ACCTATTCTCTCTCCATCTCTTCTAGCTCAGAGAACAACTTGAAGAAAAGCCCTAGATTGTGAG 7320
DB 7260 ACCTATTCTCTCTCCATCTCTTCTAGCTCAGAGAACAACTTGAAGAAAAGCCCTAGATTGTGAG 7319
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DB 7320 ATCTAGGGGGCCCTGTACTCATCTGAGCCACTTGAACCTACCTACAGATCATTCACGACTC 7379
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DB 7380 CATGGGCTTAGCGGCAATTTTCATCTCATAGTACTCTCCAGGTGAGATCAATAGGTGAGCT 7439
OY 7441 TCATGGCTCAGGAACTTGGGGTACCGCCCTTGGCAGAGTCTGAGACATCGGGCCAGAGT 7500
DB 7440 TCATGGCTCAGGAACTTGGGGTACCGCCCTTGGCAGAGTCTGAGACATCGGGCCAGAGT 7499
OY 7501 GTCCGGCTTAGGCTACTGTCTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTC 7560
DB 7500 GTCCGGCTTAGGCTACTGTCTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTC 7559
OY 7561 AACTGGGAGTAGAGACACAGCTCAAACTCACTCCATCCCGGGCTGCCAGTTCAGATTGGAT 7620
DB 7560 AACTGGGAGTAGAGACACAGCTCAAACTCACTCCATCCCGGGCTGCCAGTTCAGATTGGAT 7619
OY 7621 TTATCCAGCTGTCTCTCTCTGTACAGCGGGGAGAGACATATATACAGGCTGTCTGT 7680
DB 7620 TTATCCAGCTGTCTCTCTCTGTACAGCGGGGAGAGACATATATACAGGCTGTCTGT 7679
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DB 7680 GCCCGACCCCGGTGATGATGAGCCACTACTCTTCTGTAGAGGGGTAGGATCAT 7739
OY 7741 CTACTGCCACACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTT 7800
DB 7740 CTACTGCCACACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTT 7799
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DB 7800 TTTCCCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 7859
OY 7861 TTTTCTCTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 7920
DB 7860 TTTTCTCTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 7919
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DB 7920 TAGCGTGAAGGTCCTGAGCCGCTTGTACCTGAGAGAGTCTATACCTAGCCCTCTGCG 7979
OY 7981 AGATCAAGTACT 7992
DB 7980 AGATCAAGTACT 7991

RESULT 8
AAD25326
ID AAD25326 standard; cDNA: 7989 BP.
XX
AC AAD25326;
XX
DT 12-MAR-2002 (first entry)
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XX
DE Hepatitis C virus (HCV) adaptive replicon V mutant cDNA.
XX
KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
KW gene therapy; vaccine; immunoprotection; hepatotropic; virocid; liver;
KW adaptive replicon V; mutant; ss.
XX
OS Hepatitis C virus.
XX
FH Synthetic.
FH
FT Key Location/Qualifiers
FT CDS 4642..5982
FT /tag= a
FT /product= "NS5A variant of HCV adaptive replicon V"
FT /note= "CDS does not include both start and stop
FT codon"
FT /partial
FT mutation replace (5320, G)
FT /tag= b
XX
PN WO200189364-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-0516822.
XX
PR 23-MAY-2000; 2000US-0576989.
XX
PA (UNIM ) UNIV WASHINGTON.
XX
PI Rice CM, Blight KJ;
XX
DR MPI: 2002-066755/09.
XX
DR P-PSDB: AAL515724.
XX
PT Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences
PT
XX
PS Disclosure: page 80-83; 174pp; English.
XX
CC The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets,
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficiency replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays,
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated or defective HCV derivatives as possible vaccine candidates, engineering of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) adaptive replicon V mutant cDNA. This sequence
CC is generated by the mutation g to t at position 5320 of
CC HCVrepibBartman/Availi cDNA.
XX
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QY 2101 GGCAGCTCGAGCTTTACTTGGTCACGAGGCAATGCCGATGTCAATTCCGGTGCCTGGCG 2160
DB 2101 GGGAGCTCGAGCTTTACTTGGTCACGAGGCAATGCCGATGTCAATTCCGGTGCCTGGCGCGG 2160
QY 2161 GGGACAGCAGAGGGAGGAGCTACTCTCTCCAGAGCCCGTCTCTACTTGAAGGGCTCTCG 2220
DB 2161 GGGGACAGCAGAGGGAGGAGCTACTCTCTCCAGAGCCCGTCTCTACTTGAAGGGCTCTCG 2220
QY 2221 GGGGCTTCACACTGCTCTGCCCCCTCGGGGCAAGCTGTGGCATCTTTCCGGCTGCGCTGTC 2280
DB 2221 GGGGCTTCACACTGCTCTGCCCCCTCGGGGCAAGCTGTGGCATCTTTCCGGCTGCGCTGTC 2280
QY 2281 ACCGAGAGGGGTTGCGAAGGGGGTGAGCTTTGTACCCGTTGATGATGATGGAAGCAACTGTG 2340
DB 2281 ACCGAGAGGGGTTGCGAAGGGGGTGAGCTTTGTACCCGTTGATGATGATGGAAGCAACTGTG 2340
QY 2341 CGGTCCCGGCTCTTCACGAGCAACTGTCCCTCCGGCCGTACCCGACAGCAATTCAGGTG 2400
DB 2341 CGGTCCCGGCTCTTCACGAGCAACTGTCCCTCCGGCCGTACCCGACAGCAATTCAGGTG 2400
QY 2401 GCCCATCTACAGCCCTCTACTGTTAGCGGCAAGAGCACTAAGTCCCGCTGCGTATGCA 2460
DB 2401 GCCCATCTACAGCCCTCTACTGTTAGCGGCAAGAGCACTAAGTCCCGCTGCGTATGCA 2460
QY 2461 GCCCAAGGGTATAGGTGCTTGTCTGAAACCCGCTCCGTCGCCACCCCTAGTTTCGGG 2520
DB 2461 GCCCAAGGGTATAGGTGCTTGTCTGAAACCCGCTCCGTCGCCACCCCTAGTTTCGGG 2520
QY 2521 GCGTATATGTCTAAGGACATGTATCGACCCCTAATCATAGAACCGGGGTATGAACCATC 2580
DB 2521 GCGTATATGTCTAAGGACATGTATCGACCCCTAATCATAGAACCGGGGTATGAACCATC 2580
QY 2581 ACCAGGGGTGCCCCCATCAAGTACTCCACCTATGGCAAGTTCTTGGCGAGGTGTGTC 2640
DB 2581 ACCAGGGGTGCCCCCATCAAGTACTCCACCTATGGCAAGTTCTTGGCGAGGTGTGTC 2640
QY 2641 TCTGGGGGGGCTCTATACATCATATATATGTATGATGTCACACTCACTGACTCGACACT 2700
DB 2641 TCTGGGGGGGCTCTATACATCATATATATGTATGATGATGTCACACTCACTGACTCGACACT 2700
QY 2701 ATCTGGGAGCTGGGACAGTCCCTGAGCAAGGGAGAGCGGTGAGCGGCACTGCTGTCG 2760
DB 2701 ATCTGGGAGCTGGGACAGTCCCTGAGCAAGGGAGAGCGGTGAGCGGCACTGCTGTCG 2760
QY 2761 CTGGCCACGCTTACGCTCTCCGGGATGCTCACCGTGGCCACATCAACATGAGAGGTG 2820
DB 2761 CTGGCCACGCTTACGCTCTCCGGGATGCTCACCGTGGCCACATCAACATGAGAGGTG 2820
QY 2821 GCTCTGTCCAGCACTGTGAGAAATCCCTTTTATGGCAAAAGCCATCCCATGAGACATC 2880
DB 2821 GCTCTGTCCAGCACTGTGAGAAATCCCTTTTATGGCAAAAGCCATCCCATGAGACATC 2880
QY 2881 AAGGGGGGAGGCACTCAATTTTCTGCAATTCGAAGAAATGTGATGAGCTGCGCGG 2940
DB 2881 AAGGGGGGAGGCACTCAATTTTCTGCAATTCGAAGAAATGTGATGAGCTGCGCGG 2940
QY 2941 AAGCTGCGGGCTCGGACATCAATGTGTAGCATATTACCGGGGCTTGATGTATCCGTC 3000
DB 2941 AAGCTGCGGGCTCGGACATCAATGTGTAGCATATTACCGGGGCTTGATGTATCCGTC 3000
QY 3001 ATACCACTAGCGGAGAGCTATGTGTAGCAACGAGCGCTCTATAGCGGGCTTTACC 3060
DB 3001 ATACCACTAGCGGAGAGCTATGTGTAGCAACGAGCGCTCTATAGCGGGCTTTACC 3060
QY 3061 GGGGATTTGACTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
DB 3061 GGGGATTTGACTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
QY 3121 CTGAGCCGACCTTACACATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
DB 3121 CTGAGCCGACCTTACACATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
QY 3181 CAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240
DB 3181 CAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240
QY 3241 GAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3300
DB 3241 GAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3300
QY 3301 GCTTGGTACGAGCTACAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
DB 3301 GCTTGGTACGAGCTACAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
QY 3361 CCAGGGTCCCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
DB 3361 CCAGGGTCCCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
QY 3421 ACCGACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
DB 3421 ACCGACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
QY 3481 CTGGTACATACAGAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540
DB 3481 CTGGTACATACAGAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540
QY 3541 CAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
DB 3541 CAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
QY 3601 TATAGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
DB 3601 TATAGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
QY 3661 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720
DB 3661 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720
QY 3721 GTCCTAGCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
DB 3721 GTCCTAGCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
QY 3781 ATCATCTGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840
DB 3781 ATCATCTGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840
QY 3841 GATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
DB 3841 GATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
QY 3901 GAAATTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
DB 3901 GAAATTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
QY 3961 GCTGCTCCCGTGGTGAATCAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4020
DB 3961 GCTGCTCCCGTGGTGAATCAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4020
QY 4021 TGGAAATTTATCAGCGGGATTAACAATTTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080
DB 4021 TGGAAATTTATCAGCGGGATTAACAATTTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080
QY 4081 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140
DB 4081 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140
QY 4141 ACCCTCTCTTTAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
DB 4141 ACCCTCTCTTTAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
QY 4201 GCTTCTGCTTTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4260
DB 4201 GCTTCTGCTTTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4260
QY 4261 AAGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4320
DB 4261 AAGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4320
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4261 AAGTCTGTGGATATTTTGGCAGGTTAAGAGCAGGGGTGGCAGGGCGCTCTGGCC 4320
QY 4321 TTTAAGTTCATGAGCGCGAGATGCCCTCCACCGAGACCTGGCTAACTACTCTCTGCT 4380
DB 4321 TTTAAGTTCATGAGCGCGAGATGCCCTCCACCGAGACCTGGCTAACTACTCTCTGCT 4380
QY 4381 ATCTCTCCCTGGCGCCCTAGTCGTGCGGGGTGTGTGGCGACGCTATCTGGTGGGAC 4440
DB 4381 ATCTCTCCCTGGCGCCCTAGTCGTGCGGGGTGTGTGGCGACGCTATCTGGTGGGAC 4440
QY 4441 GTGGGCCAGGGGAGGGGGGTGTGCAGTGTATGAACCGGCTGTATGCTTCCTTCGGCG 4500
DB 4441 GTGGGCCAGGGGAGGGGGGTGTGCAGTGTATGAACCGGCTGTATGCTTCCTTCGGCG 4500
QY 4501 GGTAAACACGTCCTCCCGACGCACTATGTGCTGAGAGAGGACCTTCACACGCTGCTACT 4560
DB 4501 GGTAAACACGTCCTCCCGACGCACTATGTGCTGAGAGAGGACCTTCACACGCTGCTACT 4560
QY 4561 CAGATCCCTCTAGTCTTACCATCAGCTGCTGAGAGGCTTCACAGCTGATCAAC 4620
DB 4561 CAGATCCCTCTAGTCTTACCATCAGCTGCTGAGAGGCTTCACAGCTGATCAAC 4620
QY 4621 GAGCACTGCTCCACGCGCATGCTCGGCTCGTGAAGAGATGTTGGATTGATATGC 4680
DB 4621 GAGCACTGCTCCACGCGCATGCTCGGCTCGTGAAGAGATGTTGGATTGATATGC 4680
QY 4681 ACGGTGTTGATGATTTTCAAGACCTGCTCCAGTCCAGTCCGCGGATTCGCGGGA 4740
DB 4681 ACGGTGTTGATGATTTTCAAGACCTGCTCCAGTCCAGTCCGCGGATTCGCGGGA 4740
QY 4741 GTCCCTTCTCTCATGTCAACGTTGGGTACAGGAGTCTGGCGGGGCGACGGCATCATG 4800
DB 4741 GTCCCTTCTCTCATGTCAACGTTGGGTACAGGAGTCTGGCGGGGCGACGGCATCATG 4800
QY 4801 CAAACACCTCCCATGTGGAGCAGATATCCAGGAGATGTGAAGAAAGTTCCATGAGG 4860
DB 4801 CAAACACCTCCCATGTGGAGCAGATATCCAGGAGATGTGAAGAAAGTTCCATGAGG 4860
QY 4861 ATCGTGGGGCTAGAGACCTGTAGTAACAGTGGCATGGAACATTCCTCATTAACGGCTAC 4920
DB 4861 ATCGTGGGGCTAGAGACCTGTAGTAACAGTGGCATGGAACATTCCTCATTAACGGCTAC 4920
QY 4921 ACCAGGGCCCTGACGCGCTCCCGCGCGCAATTTATCTTAGGGGCTGTGGCGGGT 4980
DB 4921 ACCAGGGCCCTGACGCGCTCCCGCGCGCAATTTATCTTAGGGGCTGTGGCGGGT 4980
QY 4981 GCTGCTGAGAGTACGTGAGGTTACGGGGGTGGGGATTTCACATCTGACGAGGGCATG 5040
DB 4981 GCTGCTGAGAGTACGTGAGGTTACGGGGGTGGGGATTTCACATCTGACGAGGGCATG 5040
QY 5041 ACCACTGACAAAGTAAGTCCCGGTGTACGTTCCGGCCCGCGCAATTTCTTACAGAAAGT 5100
DB 5041 ACCACTGACAAAGTAAGTCCCGGTGTACGTTCCGGCCCGCGCAATTTCTTACAGAAAGT 5100
QY 5101 GATGGGGGGGGTTCACAGGTAAGTCCACAGTCCGCAAAACCGCTCCATACGGGAGAGT 5160
DB 5101 GATGGGGGGGGTTCACAGGTAAGTCCACAGTCCGCAAAACCGCTCCATACGGGAGAGT 5160
QY 5161 ACATTCTGTCGCGGCTCAATCAATACCTGTTGGGTACAGTCCCATGCGAGCCGAA 5220
DB 5161 ACATTCTGTCGCGGCTCAATCAATACCTGTTGGGTACAGTCCCATGCGAGCCGAA 5220
QY 5221 CCGGAGCTGAGAGTCTCACTTCCATGCTACGACCGCCCTCCCATTAAGGGGAGAGC 5280
DB 5221 CCGGAGCTGAGAGTCTCACTTCCATGCTACGACCGCCCTCCCATTAAGGGGAGAGC 5280
QY 5281 GCTAAGCGTGAAGCTGAGGAGATCTCCCGCTCTGCTGACAGTATACAGTAGGAG 5340
DB 5281 GCTAAGCGTGAAGCTGAGGAGATCTCCCGCTCTGCTGACAGTATACAGTAGGAG 5340
QY 5341 CTGTCTGCGGCTTCTTCAAGGCAATGCACTACCGCTATGACTCCCGGAGGCTGAC 5400
DB 5341 CTGTCTGCGGCTTCTTCAAGGCAATGCACTACCGCTATGACTCCCGGAGGCTGAC 5400

5401 CTCATGAGGCAACTCTCTGTGGCGGAGAGATGGGGGAGACATCACCCCGGTGGAG 5460
QY 5401 CTCATGAGGCAACTCTCTGTGGCGGAGAGATGGGGGAGACATCACCCCGGTGGAG 5460
DB 5401 CTCATGAGGCAACTCTCTGTGGCGGAGAGATGGGGGAGACATCACCCCGGTGGAG 5460
QY 5461 TCAGAAATATAGTATGATTTTGTGACTCTTTCAGACCCGCTCCAGCGGAGAGATGAG 5520
DB 5461 TCAGAAATATAGTATGATTTTGTGACTCTTTCAGACCCGCTCCAGCGGAGAGATGAG 5520
QY 5521 AGGGAATATCCGTTCCGGCGGAGATCTGCGGAGATCCAGGAAATTCCTTCGACGATG 5580
DB 5521 AGGGAATATCCGTTCCGGCGGAGATCTGCGGAGATCCAGGAAATTCCTTCGACGATG 5580
QY 5581 CCCATATGGGACGCGCGGATTCAGACCCCTCCACTTATGAGTCTGTAAGGACCGGAGC 5640
DB 5581 CCCATATGGGACGCGCGGATTCAGACCCCTCCACTTATGAGTCTGTAAGGACCGGAGC 5640
QY 5641 TACGTCCCTCCAGTGTACACGSGGTGCTATGCGGCTGTGCAAGGCGCTCCGATACCA 5700
DB 5641 TACGTCCCTCCAGTGTACACGSGGTGCTATGCGGCTGTGCAAGGCGCTCCGATACCA 5700
QY 5701 CTTCCAGGAGAGAGAGAGGAGGTTGCTGCTGCAAGTACAGTGTCTTCTGCTTGGCG 5760
DB 5701 CTTCCAGGAGAGAGAGAGGAGGTTGCTGCTGCAAGTACAGTGTCTTCTGCTTGGCG 5760
QY 5761 GAGCTCGCACAAAGACCTTCGAGCTCCGAATGCTGCGGCGGTGCAAGGCGCACGCA 5820
DB 5761 GAGCTCGCACAAAGACCTTCGAGCTCCGAATGCTGCGGCGGTGCAAGGCGCACGCA 5820
QY 5821 ACGGCTCTCTGACACGCGCTCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5880
DB 5821 ACGGCTCTCTGACACGCGCTCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5880
QY 5881 TCTTCATGCGCCCTTGTGAGGGGAGCGGGGATCCCATCTGACGAGGAGGCTTGG 5940
DB 5881 TCTTCATGCGCCCTTGTGAGGGGAGCGGGGATCCCATCTGACGAGGAGGCTTGG 5940
QY 5941 TCTACCGTAAGCGAGAGGCTAGTGAAGAGTGTCTGTGCTCGATGCTGATGCTGATG 6000
DB 5941 TCTACCGTAAGCGAGAGGCTAGTGAAGAGTGTCTGTGCTCGATGCTGATGCTGATG 6000
QY 6001 ACAGGCGGCTGATCAGCGCATGCGCTGCGGAGAGAAACAGCTGCCATCAATGCACTG 6060
DB 6001 ACAGGCGGCTGATCAGCGCATGCGCTGCGGAGAGAAACAGCTGCCATCAATGCACTG 6060
QY 6061 AGCAACTCTTGTCTCGCTACCAACACTTGTCTATGCTATGCTATGCTATGCTATG 6120
DB 6061 AGCAACTCTTGTCTCGCTACCAACACTTGTCTATGCTATGCTATGCTATGCTATG 6120
QY 6121 CTGGGGAGAGAGTACCTTGAACACTGAGGTTCTTGAACGACACTACCGGAG 6180
DB 6121 CTGGGGAGAGAGTACCTTGAACACTGAGGTTCTTGAACGACACTACCGGAG 6180
QY 6181 GTGCTCAAGGAGATGAAGGCGAGGCTCCAGTGAAGCTTAAGCTTAAGCTTAAGCT 6240
DB 6181 GTGCTCAAGGAGATGAAGGCGAGGCTCCAGTGAAGCTTAAGCTTAAGCTTAAGCT 6240
QY 6241 GAAAGCTGATGAGGAGGCGGCGGCTTGAAGGCTTAAGCTTAAGCTTAAGCTTAAG 6300
DB 6241 GAAAGCTGATGAGGAGGCGGCGGCTTGAAGGCTTAAGCTTAAGCTTAAGCTTAAG 6300
QY 6301 GACGTCCGGAACCTATCCAGCAAGCGGTTAACCACATCCGCTCCGTTGAGAGACTG 6360
DB 6301 GACGTCCGGAACCTATCCAGCAAGCGGTTAACCACATCCGCTCCGTTGAGAGACTG 6360
QY 6361 CTGGAAGACCTGAGACACCAATGACACCACTATGCAAGGAGGAGGAGGAGGAGG 6420
DB 6361 CTGGAAGACCTGAGACACCAATGACACCACTATGCAAGGAGGAGGAGGAGGAGG 6420
QY 6421 GTCCAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6480
DB 6421 GTCCAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6480

QY	6481	GTTCGTGTGTGCGAAGAAATGGCCCTTTACGATGTGGTCCACCCCTCCCTCAGCCGCTG	6544
Db	6481	GTTCGTGTGTGCGAAGAAATGGCCCTTTACGATGTGGTCCACCCCTCCCTCAGCCGCTG	6540
QY	6541	ATGGGCTCTTTCATACGGATTCCAACTCTCTCTGGCAGCGGGTCCGATCTCTGTGTAAT	6600
Db	6541	ATGGGCTCTTTCATACGGATTCCAACTCTCTCTGGCAGCGGGTCCGATCTCTGTGTAAT	6600
QY	6601	GCGTGGAAACGCAAGAAATAGCCCTATGGGCTTCGCAATGACACCCGCTGTTTGACTCA	6660
Db	6601	GCGTGGAAACGCAAGAAATAGCCCTATGGGCTTCGCAATGACACCCGCTGTTTGACTCA	6660
QY	6661	ACGGTCACTGAGATGACATCCGTGTTGAGAGTCGCAATCTACCAATGTTGTGACTGGCC	6720
Db	6661	ACGGTCACTGAGATGACATCCGTGTTGAGAGTCGCAATCTACCAATGTTGTGACTGGCC	6720
QY	6721	CCCGAACCAGACAGGCCATTAAGTGGCTCACAGAGCGGCTTTACATGGGGGCCCCCTG	6780
Db	6721	CCCGAACCAGACAGGCCATTAAGTGGCTCACAGAGCGGCTTTACATGGGGGCCCCCTG	6780
QY	6841	ACCAAGCTGCGGTATACCCCTACATCTTACTTGAAGGCGCTGCGGCCCTGTGCACTGCG	6900
Db	6841	ACCAAGCTGCGGTATACCCCTACATCTTACTTGAAGGCGCGTGTGCACTGCG	6900
QY	6901	AAGCTCCAGACCTGCAAGATGCTCTGATACCGGAGACAGACTTGTGTTATCTGGAAGC	6960
Db	6901	AAGCTCCAGACCTGCAAGATGCTCTGATACCGGAGACAGACTTGTGTTATCTGGAAGC	6960
QY	6961	GCGGGGACCCCAAGAGCGAGCGGACCTACGGGCTTCACGAGGCTATGACTAGATAC	7020
Db	6961	GCGGGGACCCCAAGAGCGAGCGGACCTACGGGCTTCACGAGGCTATGACTAGATAC	7020
QY	7021	TCGTGCCCCCTTGGGAGCCCGGCCAAACCGACATAGCATTTGGATGTATATCAATCATGC	7080
Db	7021	TCGTGCCCCCTTGGGAGCCCGGCCAAACCGACATAGCATTTGGATGTATATCAATCATGC	7080
QY	7081	TCTCCCAATGTGTCAGTGCGGCGACGATGTCATGTGGCAAAAGGGTGTACTATCTCACCGGT	7140
Db	7081	TCTCCCAATGTGTCAGTGCGGCGACGATGTCATGTGGCAAAAGGGTGTACTATCTCACCGGT	7140
QY	7141	GACCCCAACACCCCTTGGGCGGGCTGGGTGGGAGACGCTAAGACACACTCCAGCTCAAT	7200
Db	7141	GACCCCAACACCCCTTGGGCGGGCTGGGTGGGAGACGCTAAGACACACTCCAGCTCAAT	7200
QY	7201	TCTCGGCTAGGCAACATCAATCATGTATGCGCCACCTGTTGGGCAAGGATGATCTGTATG	7260
Db	7201	TCTCGGCTAGGCAACATCAATCATGTATGCGCCACCTGTTGGGCAAGGATGATCTGTATG	7260
QY	7261	ACTATATTCTTCTCCACCTTCTAGCTCAAGAACTTGAAAAAGCCCTGATATTGTACG	7320
Db	7261	ACTATATTCTTCTCCACCTTCTAGCTCAAGAACTTGAAAAAGCCCTGATATTGTACG	7320
QY	7321	ATTCACGGGGCTGTGTACTCCATTGAGCACTTGACCTACCTCAGATCATTCACGACTC	7380
Db	7321	ATTCACGGGGCTGTGTACTCCATTGAGCACTTGACCTACCTCAGATCATTCACGACTC	7380
QY	7381	CATGGCCCTTACCGGATTTCACCTAGTACTCTCCAGGAGATCAATAGGGTGGCT	7440
Db	7381	CATGGCCCTTACCGGATTTCACCTAGTACTCTCCAGGAGATCAATAGGGTGGCT	7440
QY	7441	TCATGCTCAGAAACTTGGGGTACCGCCCTTGGAGTCTGAGACATCGGGCCAGAAAT	7500
Db	7441	TCATGCTCAGAAACTTGGGGTACCGCCCTTGGAGTCTGAGACATCGGGCCAGAAAT	7500
QY	7501	GTCGCGCTTAGGCTACTGTGCCACAGGGGGAGGAGGCTGCACACTTGTGGCAAGTACTCTTC	7560
Db	7501	GTCGCGCTTAGGCTACTGTGCCACAGGGGGAGGAGGCTGCACACTTGTGGCAAGTACTCTTC	7560
QY	7561	AACCTGGGAGTAAAGACCAAGCTCAAACTCAATCCCGGCTGCTCCAGTTGGAT	7620

Db	7561	AACGGGCGACGTAGAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTCGCTCCAGTTGGAT	7620
Qy	7621	TTATCCAGCTGGTTCGTGCTGCTGGTTACAGCGGGGAGACATATATCAGAGCTGTCTCGT	7680
Db	7621	TTATCCAGCTGGTTCGTGCTGCTGGTTACAGCGGGGAGACATATATCAGAGCTGTCTCGT	7680
Qy	7681	GCCCGACCCCGCTGGTTGATGTGTGCTACTCTACTCTTCTGTAGGGGTAGGCATCTAT	7740
Db	7681	GCCCGACCCCGCTGGTTGATGTGTGCTACTCTACTCTTCTGTAGGGGTAGGCATCTAT	7740
Qy	7741	CTATCCCGCCACCGATGAGACGGGGAGCTTAACATCCAGGCGCATPAGGCATCCTGTTT	7800
Db	7741	CTATCCCGCCACCGATGAGACGGGGAGCTTAACATCCAGGCGCATPAGGCATCCTGTTT	7800
Qy	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Qy	7861	TTTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	7861	TTTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Qy	7921	TAGCTGTGAAGGTCGGTGTAGCGGCTTGACTGTGACTGCAGAGAGTCTGATACTAGGCTCTCTGC	7980
Db	7921	TAGCTGTGAAGGTCGGTGTAGCGGCTTGACTGTGACTGCAGAGAGTCTGATACTAGGCTCTCTGC	7980
Qy	7981	AGATCAAGT 7989	
Db	7981	AGATCAAGT 7989	
RESULT 9			
ID	AAD25325		
AD	AAD25325 standard; cDNA; 7989 BP.		
AC	AAD25325;		
DT	12-MAR-2002 (first entry)		
DE	Hepatitis C virus (HCV) adaptive replicon II CDNA mutant.		
XX			
XX	Hepatitis C virus; HCV; transfection; infection; virus neutralisation;		
XX	gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver		
XX	adaptive replicon II; mutant; ss.		
XX			
OS	Hepatitis C virus.		
XX	Synthetic.		
XX			
XX			
XX	Key	Location/Qualifiers	
XX	CDS	1801..7758	
XX	FT	/*tag- a	
XX	FT	/product- "HCV adaptive replicon II proteIn"	
XX	FT	4642..5982	
XX	CDS	/*tag- b	
XX	FT	/product- "NS5a protein of HCV adaptive replicon II"	
XX	FT	/note- "CDS does not include both start and stop	
XX	FT	codon"	
XX	FT	/partial	
XX			
XX	MO200189364-A2.		
XX	29-NOV-2001.		
XX			
XX	23-MAY-2001; 2001MO-US16822.		
XX			
XX	23-MAY-2000; 2000US-0576989.		
XX			
XX	(UNIW) UNIV WASHINGTON.		
XX			
XX	Rice CM, Blight KJ;		
XX			
XX	WPI; 2002-066755/09.		

DR P-PSDB; AAE15722, AAE15723.

PT Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences

Example 1; Page 77-80; 174pp; English.

The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive passagage greater than HCV that have wild-type polypeptide coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for the generation of defined HCV stocks to develop in vitro and in vivo assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficiency replication in cell culture, production of HCV variants with altered tissue or species tropism, establishment of alternative animal models for inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated HCV derivatives as possible vaccine candidates, engineering of attenuated or defective HCV derivatives for expression of heterologous gene products for gene therapy and vaccine applications and for utilisation of the HCV glycoproteins for targeted delivery of therapeutic agents to the liver or other cell types with appropriate receptors. Vaccine comprising these sequences is useful for inducing immunoprotection to HCV in a primate. The present sequence is Hepatitis C virus (HCV) adaptive replicon in cDNA mutant. This sequence is generated by the mutation a to g at position 5289 of HCVrep1Bartman/Avail cDNA.

Sequence 7989..BP; 1644 A; 2369 C; 2245 G; 1731 T; 0 other;

Query Match	99.8%;	Score 7976.2;	DB 24;	Length 7989;
Best Local Similarity	99.9%;	Pred. No. 0;		

Matches 7981; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	1	GGCAGCCCCCGATTGGGGGGCAGCACTCCACCATATGATCACTCCCTGTGAGAGAACTACTG	60
Db	1	GGCAGCCCCCGATTGGGGGGCAGCACTCCACCATATGATCACTCCCTGTGAGAACTACTG	60
QY	61	TCTTCAGCAGAAAGCGTCTAGCGCATGGCGTTAGTATGATGTCGTGGACGCTCCAGAC	120
Db	61	TCTTCAGCAGAAAGCGTCTAGCGCATGGCGTTAGTATGATGTCGTGGACGCTCCAGAC	120
QY	121	CCCCCCTCCCGGGAGAGCCATAGTGTCTCGGACACGGGTAGTACACCGAATTCGCAG	180
Db	121	CCCCCCTCCCGGGAGAGCCATAGTGTCTCGGACACGGGTAGTACACCGAATTCGCAG	180
QY	181	GAGACACGGGTCCTTTCTTGATATACCCGCTAATGCTCGAGATTTGGGCGTGGCCCC	240
Db	181	GAGACACGGGTCCTTTCTTGATATACCCGCTAATGCTCGAGATTTGGGCGTGGCCCC	240
QY	241	GGCAGACCTCTAGCCGAGTATGTTGGTGGCGCAAGGGCTGTGTACTCCGTATAGG	300
Db	241	GGCAGACCTCTAGCCGAGTATGTTGGTGGCGCAAGGGCTGTGTACTCCGTATAGG	300
QY	301	GTCCTTGGCAGATGCCCGGGAGGTCTGTGTAGACGTGACACATGAGACGAATCTTAAC	360
Db	301	GTCCTTGGCAGATGCCCGGGAGGTCTGTGTAGACGTGACACATGAGACGAATCTTAAC	360
QY	361	CTTAAGGAAAAACCAAAGGCGCGCCATGATTAACAAAGATGAGATTGCAACGAGTTCTC	420
Db	361	CTTAAGGAAAAACCAAAGGCGCGCCATGATTAACAAAGATGAGATTGCAACGAGTTCTC	420

QY	421	CGCCGCTTGGGTGAGAGGCTATTTGGCATATACATGGGCGACAAACAGAAATCGGCTCT	480
Db	421	CGCGCGCTTGGGTGAGAGGCTATTTGGCATATACATGGGCGACAAACAGAAATCGGCTCT	480
QY	481	CTGATGCCGCCGTTTCGGGCTGTGACGCGAGGGGCGCCCGGTTCTTTTGTCAAGACCG	540
Db	481	CTGATGCCGCCCTGTTCGGGCTGTGACGCGAGGGGCGCCCGGTTCTTTTGTCAAGACCG	540
QY	541	ACCGTCCGGGTGGCCCTAATGACATCGAGACGAGGCGACGGGGCATCGTGTGGCTGGCA	600
Db	541	ACCGTCCGGGTGGCCCTAATGAACTGAGGACGAGGCGACGGGGCATATGTGTGGCTGCA	600
QY	601	CGAGGGGGGTTTCCTTGGCGACGCTGTGTCACGTTTCTACTGAAGCGGGAAGGACTGGC	660
Db	601	CGAGGGGGGTTCTTGGCGAGCTGTGTCGACGTTTGTCTACTGAAGCGGGAAGGACTGGC	660
QY	661	TGCTATTGGGGGAAGTCCCGGGGCGAGGATTCCTGTCACTCACTCACTTCCTGCTGGCAGA	720
Db	661	TGCTATTGGGGGAAGTCCCGGGGAGGATTCCTGTCACTCACTCACTTCCTGCTGGCAGA	720
QY	721	AAGTATCCATCATGCTGATGCAATGGCGCGCTGCATACGTTGATCCGCGCTACTCGC	780
Db	721	AAGTATCCATCATGCTGTGATGCAATGGCGCGCTGCATACGTTGATCCGCGCTACTCGC	780
QY	781	CATTGAGACCACCAAGGGAACATCGATCGAGGACAGCTACTGTGATGGAAGCGCGGTC	840
Db	781	CATTGAGACCACCAAGGGAACATCGATCGAGGACAGCTACTGTGATGGAAGCGCGGTC	840
QY	841	TTGTGATCAGAGTATCTGAGAGGAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTGC	900
Db	841	TTGTGATCAGAGTATCTGAGAGGAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTGC	900
QY	901	CCAGGCTCAAGGGCGCGCATCCCGAGCGCGAGATTCGTGTCGACCATGGCGATGGCT	960
Db	901	CCAGGCTCAAGGGCGCGCATCCCGAGCGAGGATTCGTGTCGACCATGGCGATGGCT	960
QY	961	GCTTGCAGAAATATCATGTTGGAATAATGGCCGCTTTTCTGGAATTCATCGACTGTGGCGCG	1020
Db	961	GCTTGCAGAAATATCATGTTGGAATAATGGCCGCTTTTCTGGAATTCATCGACTGTGGCGCG	1020
QY	1021	TGGGTGAGGGGAGCCGCTATCAGAGACATGAGCGTTGGCTACCCGTAATATGGCTGAAGAGC	1080
Db	1021	TGGGTGAGGGGAGCCGCTATCAGAGACATGAGCGTTGGCTACCCGTAATATGGCTGAAGAGC	1080
QY	1081	TTTGGGCGGAATGGGCTGACCGCGTTCCTGCTTAAAGATATGCGCCGCTCCGATTTGCG	1140
Db	1081	TTTGGGCGCGAATGGGCTGACCGCGTTCCTGCTTAAAGATATGCGCCGCTCCGATTTGCG	1140
QY	1141	AGGCGATCGGCTTCTATCGGCTTCTGAGAGATCTCTTGAGATTTAAACAGACCCAGAGC	1200
Db	1141	AGGCGATCGGCTTCTATCGGCTTCTGAGAGATCTCTTGAGATTTAAACAGACCCAGAGC	1200
QY	1201	GTTTCCCTCTAGCGGGGATCAATTCCGCCCTCTCCCTCCGCCCCCTTAACGTTACTGGC	1260
Db	1201	GTTTCCCTCTAGCGGGGATCAATTCCGCCCTCTCCCTCCGCCCCCTTAACGTTACTGGC	1260
QY	1261	CGAAGCCGCTTGGATTAAGCCCGGTGGGTTGTATATATATATTTTCCACCACTATTG	1320
Db	1261	CGAAGCCGCTTGGATTAAGCCCGGTGGGTTGTCTATATATATATTTTCCACCACTATTG	1320
QY	1321	CCGTCCTTTTGGCAATGTGAGGGCCCGGAAACCTGCGCCCTGTCTTTCAGCAGCAATTCT	1380
Db	1321	CCGTCCTTTTGGCAATGTGAGGGCCCGGAAACCTGCGCCCTGTCTTTCAGCAGCAATTCT	1380
QY	1381	AGGGGTCTTTTCCCTCTCGCCCAAGGAATGCAAGGCTGTGTAATGTGTGAAGGAACA	1440
Db	1381	AGGGGTCTTTTCCCTCTCGCCCAAGGAATGCAAGGCTGTGTAATGTGTGAAGGAACA	1440
QY	1441	GTTCTCTGAGACCTCTTGAAGACAACAACAGCTGTGAGAGCCCTTTGACAGCGAGCGG	1500
Db	1441	GTTCTCTGAGACCTCTTGAAGACAACAACAGCTGTGAGAGCCCTTTGACAGCGAGCGG	1500

QY	1501	AA	CCCCCACCCTGGCGACAGTGCCTCTGGGGCAAAACCCAGCGTTATAGATACACT	1560
Db	1501	AA	CCCCCACCCTGGCGACAGTGCCTCTGGGGCAAAACCCAGCGTTATAGATACACT	1560
QY	1561	GCA	AGGCGGGCACAAACCCAGTGCACGTTGTAGATAGTTGTGGAAAGAGTCAAA	1620
Db	1561	GCA	AGGCGGGCACAAACCCAGTGCACGTTGTAGATAGTTGTGGAAAGAGTCAAA	1620
QY	1621	TGG	CTCTCCATCAAGCGATATCAACAAGGGGGTGAAGAGATGCCACAGATGCCCATATGT	1680
Db	1621	TGG	CTCTCTCCATCAAGCGATATCAACAAGGGGGTGAAGAGATGCCACAGATGCCCATATGT	1680
QY	1681	ATG	GGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGtGTTAATCGAGTTAAA	1740
Db	1681	ATG	GGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGtGTTAATCGAGTTAAA	1740
QY	1741	AAC	CTTAGGGCCCCCGCAACACAGGGGAGTGGTTCTCTTGA AAAACAGATATATCC	1800
Db	1741	AAC	CTTAGGGCCCCCGCGAACACAGGGGAGTGGTTCTCTTGA AAAACAGATATATCC	1800
QY	1801	ATG	CGCGCTATTAGGCGCTACTGCCAACAGACCGCAGGCGCTACTTGCTGCATCATCT	1860
Db	1801	ATG	CGCGCTATTAGGCGCTACTGCCAACAGACCGCAGGCGCTACTTGCTGCATCATCT	1860
QY	1861	AGC	CTCAGAGCCGGGACAGAGAACAGAGTGCAGAGGGGAGATGCAGATGGTCCACGCA	1920
Db	1861	AGC	CTCAGACAGCCGGGACAGAGAACAGAGTGCAGAGGGGAGATGCAGATGGTCCACGCA	1920
QY	1921	ACACA	TCTTTCTGGCGAGCTCGCTCAATGGCGTGTGTGGACTGTCTATCATGTGTC	1980
Db	1921	ACACA	TCTTTCTGGCGAGCTCGCTCAATGGCGTGTGTGGACTGTCTATCATGTGTC	1980
QY	1981	GGC	TCAAGAACCCTTGGCGGCCCAAGAGGGCGCCATACCCAATGTACACCATGTGAC	2040
Db	1981	GGC	TCAAGAACCCTTGGCGGCCCAAGAGGGCGCCATACCCAATGTACACCATGTGAC	2040
QY	2041	CAG	ACTCTGGGTGGCAAGCGCCCCCGGGGCGCTTCTTGACACATGCACCTGC	2100
Db	2041	CAG	ACTCTGGGTGGGTGGCAAGCGCCCCCGGGGCGCTTCTTGACACATGCACCTGC	2100
QY	2101	GGA	AGCTCGACCTTACTTGTGCAGAGGATGCAGATGCATATTCGGTGGCGGCGG	2160
Db	2101	GGA	AGCTCGACCTTACTTGTGCAGAGGATGCAGATGCATATTCGGTGGCGGCGG	2160
QY	2161	GGA	AGCTCGACCTTACTTGTGCAGAGGATGCAGATGCATATTCGGTGGCGGCGG	2160
Db	2161	GGA	AGCTCGACCTTACTTGTGCAGAGGATGCAGATGCATATTCGGTGGCGGCGG	2160
QY	2221	GGA	AGCTCGACCTTACTTGTGCAGAGGATGCAGATGCATATTCGGTGGCGGCGG	2280
Db	2221	GGA	AGCTCGACCTTACTTGTGCAGAGGATGCAGATGCATATTCGGTGGCGGCGG	2280
QY	2281	ACC	GAGGGGTGGGAAGGGGGTGAAGCTTGTACCCGTGCAGATCATGGA AACCACTATG	2340
Db	2281	ACC	GAGGAGGGGTGGGAAGGGGGTGAAGCTTGTACCCGTGCAGATCATGGA AACCACTATG	2340
QY	2341	CGT	CTCCCGGCTTTCACGACCAACTCGTCCCTCGGGCGGTACCGACATTTCCAGGTG	2400
Db	2341	CGT	CTCCCGGCTTTCACGACCAACTCGTCCCTCGGGCGGTACCGACATTTCCAGGTG	2400
QY	2401	GCC	ATCTACACGGCCCTACTGGTAGCGGACAGAGACTTAAGSTGCCGGCTGCATATGCA	2460
Db	2401	GCC	ATCTACACGGCCCTACTGGTAGCGGACAGAGACTTAAGSTGCCGGCTGCATATGCA	2460
QY	2461	GCC	ATCTACACGGCCCTACTGGTAGCGGACAGAGACTTAAGSTGCCGGCTGCATATGCA	2460
Db	2461	GCC	ATCTACACGGCCCTACTGGTAGCGGACAGAGACTTAAGSTGCCGGCTGCATATGCA	2460
QY	2521	GCG	ATATGTCTAAGGACATGTGTATCGAACCCATAATAGAACGGGGTATAGGACATTC	2580
Db	2521	GCG	ATATATGTCTAAGGACATGTGTATCGAACCCATAATAGAACGGGGTATAGGACATTC	2580
QY	2581	ACA	CGAGGTGCCCCATCAGTACTCCACCTATGGCAGAGTTCTTCCGACCGGTGTC	2640
Db	2581	ACA	CGAGGTGCCCCATCAGTACTCCACCTATGGCAGAGTTCTTCCGACCGGTGTC	2640

Db	2581	ACACGGGTGCCCCCACTACGCTACTCCACCTATGGAAATTTCTTGCCGAGGTTGTTGC	2640
Qy	2641	TCGTGGGGCGCTATGACATCATATAATATGTGATGAGTGGCACTCACTGACTCGACACT	2700
Db	2641	TCGTGGGGCGGCTATGACATCATATAATATGATGAGTGGCACTCACTGACTCGACACT	2700
Qy	2701	ATCCGGGCAATCGGCACAGTCTCTGAGCAAGAGGAGACGGGTGGAGCGGATCGTCTG	2760
Db	2701	ATCCGGGCAATCGGCACAGTCTCTGAGCAAGAGGAGACGGGTGGAGCGGATCGTCTG	2760
Qy	2761	CTCGCCACCGCTACGCTCCGGGATCGTGACCGTGCACATCCAAACATCGAGGAGTG	2820
Db	2761	CTCGCCACCGCTACGCTCCGGGATCGTGACCGTGCACATCCAAACATCGAGGAGTG	2820
Qy	2821	GCTCTGTCACACCTATGGAATAATCCCTTTATGGCAAGCCATCCCATCGAGACATC	2880
Db	2821	GCTCTGTCACACCTATGGAATAATCCCTTTATGGCAAGCCATCCCATCGAGACATC	2880
Qy	2881	AAGGGGGGAGGACACTCATTTTCTGCACTCCAGAGAAATGTGATAGCTGGCGCG	2940
Db	2881	AAGGGGGGAGGACACTCATTTTCTGCACTCCAGAGAAATGTGATAGCTGGCGCG	2940
Qy	2941	AAGCTGTCCGGCTCGGACACTCAATGCTGTGACATATACCGGGGCTGATATACGTC	3000
Db	2941	AAGCTGTCCGGCTCGGACACTCAATGCTGTGACATATACCGGGGCTGATATACGTC	3000
Qy	3001	ATACCACTATGCGGAGACGTCATTTGTGTGACAGGACGCTCTATGACGAGGCTTTAC	3060
Db	3001	ATACCACTATGCGGAGACGTCATTTGTGTGACAGGACGCTCTATGACGAGGCTTTAC	3060
Qy	3061	GAGCATTTGCGACTAGTATGCACTGCAATACATGTGTACACCAACAGTGCAGCTTACG	3120
Db	3061	GAGCATTTGCGACTAGTATGCACTGCAATACATGTGTACACCAACAGTGCAGCTTACG	3120
Qy	3121	CTGACCCCGACCTTACACCATTTAGAGAGAGAGACCGGTGCCCAAGACGGCGTGTACGCTG	3180
Db	3121	CTGACCCCGACCTTACACCATTTAGAGAGAGAGACCGGTGCCCAAGACGGCGTGTACGCTG	3180
Qy	3181	CAGCGCGAGGACAGACTGATAGGAGGAGAGATGGGATTTAAGGTTTGTGACTCCAGA	3240
Db	3181	CAGCGCGAGGACAGACTGATAGGAGGAGAGATGGGATTTAAGGTTTGTGACTCCAGA	3240
Qy	3241	GACGCGCCCTCGGCAATGTCGAAATCTCGTCTGTGGGAATGCTATGACGCGGGCGT	3300
Db	3241	GACGCGCCCTCGGCAATGTCGAAATCTCGTCTGTGGGAATGCTATGACGCGGGCGT	3300
Qy	3301	GCTTGCTAGAGCTCACGCGCCGCGGACCTCAGTTAGTTTCGGGCTTACCTAAACACA	3360
Db	3301	GCTTGCTAGAGCTCACGCGCCGCGGACCTCAGTTAGTTTCGGGCTTACCTAAACACA	3360
Qy	3361	CGAGGTTGGCCCGTCTGCGAGGACATCTGGAATTTGGGAAGGGTCTTTACAGCCCTC	3420
Db	3361	CGAGGTTGGCCCGTCTGCGAGGACATCTGGAATTTGGGAAGGGTCTTTACAGCCCTC	3420
Qy	3421	ACCCACATAGACGCCATTTCTTGTGTCAGACTAAGCAGGCAAGAGACAATTCCTCTAC	3480
Db	3421	ACCCACATAGACGCCATTTCTTGTGTCAGACTAAGCAGGCAAGAGACAATTCCTCTAC	3480
Qy	3481	CTGGAGATATCCAGGGCTAGGAGTGGGGCCAGGAGCTCAAGCTCACTACGTGGGAC	3540
Db	3481	CTGGAGATATCCAGGGCTAGGAGTGGGGCCAGGAGCTCAAGCTCACTACGTGGGAC	3540
Qy	3541	CAATGTGAGAGTGTCTCATACGGCTAAGGCTACGCTGCACGGGCAAGCCCTCTGCTG	3600
Db	3541	CAATGTGAGAGTGTCTCATACGGCTAAGGCTACGCTGCACGGGCAAGCCCTCTGCTG	3600
Qy	3601	TATAGCTGGAGCGCTTCAAAAGAGAGTTACTACACACACCCCATAAACAAATATATC	3660
Db	3601	TATAGCTGGAGCGCTTCAAAAGAGAGTTACTACACACACCCCATAAACAAATATATC	3660
Qy	3661	ATTGCATGATGTGCGCTGACCTGGAAGTGTGCAGAGCACTGGGTGCTGATGCGGA	3720

Db	3661	ATGGCATGCATGTGGGCTGACCTGGAGGTGTCACAGCACCTGGGTCGTGTGAAGCGGA	3720
Qy	3721	GTCCCTACACCTGTGGCGCGGTATTTGTCCTGACACAGGACGGTGTGATTTGTGGCGAG	3780
Db	3721	GTCCCTACACCTGTGGCGCGGTATTTGTCCTGACACAGGACGGTGTGATTTGTGGCGAG	3780
Qy	3781	ATCATCTTTCGGGAAGGCCGSCATATTCGCCGACAGGGAAGTCTTTACCGGAGTTC	3840
Db	3781	ATCATCTTTCGGGAAGGCCGSCATATTCGCCGACAGGGAAGTCTTTACCGGAGTTC	3840
Qy	3841	GATAGATGGAAAGTGGCGCTCACACCTCCCTTCATGAACAGGGAATCAGCTCGCC	3900
Db	3841	GATAGATGGAAAGTGGCGCTCACACCTCCCTTCATGAGAACAGGAATCAGCTCGCC	3900
Qy	3901	GAACAAATTCAACAGAAAGGCATCGGGTTGCTGCACAAACCCACCAAGCAAGCGAGCT	3960
Db	3901	GAACAAATTCAACAGAAAGGCATCGGGTTGCTGCACAAACCCACCAAGCGAGCT	3960
Qy	3961	GCTGCTCCGCGTGGGGAATCAGTGGGGACCCCTGGAAGCCTTCTGGGCGAAGCATATG	4020
Db	3961	GCTGCTCCGCGTGGGGAATCAGTGGGGACCCCTGGAAGCCTTCTGGGCGAAGCATATG	4020
Qy	4021	TGGAATTCATACAGCGGATACAAATATTAGACAGGCTTTCACATCTGCTGGCAACCC	4080
Db	4021	TGGAATTCATACAGCGGATACAAATATTAGAGAGCTTTCACATCTGCTGGCAACCC	4080
Qy	4081	GGCATAGCATACAGTAGGCATTACAGGCTCTATATACAGCGCGCTCACCAACCCAAAT	4140
Db	4081	GGCATAGCATACAGTAGGCATTACAGGCTCTATATACAGCGCGCTCACCAACCCAAAT	4140
Qy	4141	ACCCTCGTTTAACATCTGCGGGGGGTGGGTGGCGCCCAACTGTGCTTCCACGCGCT	4200
Db	4141	ACCCTCGTTTAACATCTGCGGGGGGTGGGTGGCGCCCAACTGTGCTTCCACGCGCT	4200
Qy	4201	GCTTCTGCTTTCGTAGCGCGCGCATGCTGTGAAGCGGCTGTGTGCAGCATAGGCTTGGG	4260
Db	4201	GCTTCTGCTTTCGTAGCGCGCGCATGCTGTGAAGCGGCTGTGTGCAGCATAGGCTTGGG	4260
Qy	4261	AAGGTGCTTGAGATTTTGGCAGGTTATGAGACAGGGGTGGCAGGCGCTGCTGGCC	4320
Db	4261	AAGGTGCTTGAGATTTTGGCAGGTTATGAGACAGGGGTGGCAGGCGCTGCTGGCC	4320
Qy	4321	TTTAAGGTCATGACGCGCGAGATGCCCTCCACGAGGACCTTGGCTACTACTCCCTGCT	4380
Db	4321	TTTAAGGTCATGACGCGCGAGATGCCCTCCACGAGGACCTTGGTAACTACTCCCTCT	4380
Qy	4381	ATCCCTCCCTTGCGCGCCTAGTGTGAGGGGTGTGTGGCAGACGATATGTGCTGGGAC	4440
Db	4381	ATCTCTCCCTTGCGCGCCTAGTGTGTGGGGGTGTGTGGCAGCATATCTGGTGGGAC	4440
Qy	4441	GTGGGCCCAAGGGAAGGGGCTGTGTGCAGTGATGAACCGGCTGTATAGCTTGGCTTCGGG	4500
Db	4441	GTGGGCCCAAGGGAAGGGGCTGTGTGCAATGATGAACCGGCTGTATAGCTTGGCTTCGGG	4500
Qy	4501	GCTAACCAAGTCTCCCCACAGCACTATATGTGCCCGACAGGAGCTGACACAGTGTACT	4560
Db	4501	GCTAACCAAGTCTCCCCACAGCACTATATGTGCTGTGAAGGAGCTGTACACAGTGTACT	4560
Qy	4561	CAGATCCCTCTAGTCTTACATCACTACAGCTCTCAAGAGGCTTACCAAGTGTATCAAC	4620
Db	4561	CAGATCCCTCTGTGTCTTACATCACTACAGCTCTGTGAAGGCTTACCAAGTGTATCAAC	4620
Qy	4621	GAGGACTGCTCCAGGCCATGCTCCGGCTGTGGCTTAAGAGATTTTGGATTGGATATGC	4680
Db	4621	GAGGACTGCTCCAGGCCATGCTCCGGCTGTGGCTTAAGAGATTTTGGATTGGATATGC	4680
Qy	4681	ACGGATTGACGTATTTCAACAACTGGCTCAGTCCAAAGTCTCTGGCGGGATTCCGGGGA	4740
Db	4681	ACGGATTGACGTATTTCAACAACTGGCTCAGTCCAAAGTCTCTGGCGGGATTCCGGGGA	4740
Qy	4741	GTCCCTTCTTCATGTCACAGTGGTACAGGGAGTCTGCGGGGCGACGGCATATG	4800
Db	4741	GTCCCTTCTTCATGTCACAGTGGTACAGGGAGTCTGCGGGGCGACGGCATATG	4800

QY	4801	CAAAACACCTTCCCATATGTGGACGACACGATACCGGACATGTGTAATAAAAGGTTCCATAGC	4860
Db	4801	CAAAACACCTTCCCATATGTGGACGACGATACCGGACATGTGTAATAAAAGGTTCCATAGC	4860
QY	4861	ATCGTGGGCGCTTAGGACCTTAGTAAACAGTGGCATGAGAACATTTCCCATTAAGCGTAC	4920
Db	4861	ATCGTGGGCGCTTAGGACCTTAGTAAACAGTGGCATGAGAACATTTCCCATTAAGCGTAC	4920
QY	4921	ACCAAGGGCCCTCAGCGCCCTCCCGGGGCCAATATTCTAAGGCGCTGTGGCGGTG	4980
Db	4921	ACCAAGGGCCCTCAGCGCCCTCCCGGGGCCAATATTCTAAGGCGCTGTGGCGGTG	4980
QY	4981	GCTGCTAGAGAGTACGTGAGAGTTTACGGGGTGGGGGATTTCCACTAGGTGACGGGATG	5040
Db	4981	GCTGCTAGAGAGTACGTGAGAGTTTACGGGGTGGGGGATTTCCACTAGGTGACGGGATG	5040
QY	5041	ACCACTGACAACTGAAGTGCCTGTCAGGTTCCGGCCCCCGAATTTCTTACAGAAATG	5100
Db	5041	ACCACTGACAACTGAAGTGCCTGTCAGGTTCCGGCCCCCGAATTTCTTACAGAAATG	5100
QY	5101	GATGGGTTGCAGGTTCACAGGTACGCTCCAGCTGCAAAACCCCTCTACGGGAGAGTGC	5160
Db	5101	GATGGGTTGCAGGTTCACAGGTACGCTCCAGCTGCAAAACCCCTCTCTACGGGAGAGTGC	5160
QY	5161	ACATTCTTGGTGGGCTCATCAATACCTTGGTGGTGCACAGCTCCCATGGAGCCGAA	5220
Db	5161	ACATTCTTGGTGGGCTCATCAATACCTTGGTGGTGCACAGCTCCCATGGAGCCGAA	5220
QY	5221	CCGACGTAAGAGTGTCTACTCTCATGCTCACGACCCCTCCACATTAACGGCGAGAGC	5280
Db	5221	CCGACGTAAGAGTGTCTACTCTCATGCTCACGACCCCTCCACATTAACGGCGAGAGC	5280
QY	5281	GCTAAGCCTAAGGCGGGCGAGGGATCTCCCCCTCCTTGGCAGGCAATACAGTACGAG	5340
Db	5281	GCTAAGCCTAAGGCGGGCGAGGGATCTCCCCCTCCTTGGCAGGCAATACAGTACGAG	5340
QY	5341	CTGTGTGCGCCTTCTTGAAGGCAACATGACATCCGTCATGACTCCCCGGACGCTGAC	5400
Db	5341	CTGTGTGCGCCTTCTTGAAGGCAACATGACATCCGTCATGACTCCCCGGACGCTGAC	5400
QY	5401	CTCATCGAGGCGCAACCTCTGTGGCGGCGAGAGATGGGGGGGAATATCAACCCGCTGGAG	5460
Db	5401	CTCATCGAGGCGCAACCTCTGTGGCGGCGAGAGATGGGGGGGAATATCAACCCGCTGGAG	5460
QY	5461	TCAGAAATTAAGTAGTATTAATTTTGACTTTTCGAGCCGCTCCAAACGGAGAGATAG	5520
Db	5461	TCAGAAATTAAGTAGTATTAATTTTGACTTTTCGAGCCGCTCCAAACGGAGAGATAG	5520
QY	5521	AAGGAAGTATCCGTTCCGGGGGAGATCTGTGGAGGCCAGGAATTTCCCTGAGACGATG	5580
Db	5521	AAGGAAGTATCCGTTCCGGGGGAGATCTGTGGAGGCCAGGAATTTCCCTGAGACGATG	5580
QY	5581	CCCATATGAGGACGCGCGGATTTACAACTCTCACTGTTAAGTCTTGAAGGACCCGGAC	5640
Db	5581	CCCATATGAGGACGCGCGGATTTACAACTCTCACTGTTAAGTCTTGAAGGACCCGGAC	5640
QY	5641	TACGTCCTCCAGTGGTACAGAGGTTGCTAFTGGCGCTGACCAAGGCCCTCCGATACCA	5700
Db	5641	TACGTCCTCCAGTGGTACAGAGGTTGCTAFTGGCGCTGACCAAGGCCCTCCGATACCA	5700
QY	5701	CCTCCACGAGAGAGGACGCGTTGTCTGTCAAAATCTACGCTGTCTTTCGCTTGGCG	5760
Db	5701	CCTCCACGAGAGAGAGGACGCGTTGTCTGTCAAAATCTACGCTGTCTTTCGCTTGGCG	5760
QY	5761	GAGCTGCGACAAACCTTTGGGAGTCCGAATTCGTCGAGCCCTGCACAGCGGACGCGCA	5820
Db	5761	GAGCTGCGACAAACCTTTGGGAGTCCGAATTCGTCGAGCCCTGCACAGCGGACGCGCA	5820
QY	5821	ACGCGCTCTCTGACACGACCTCTCGACGACGGGAGCGCGAGATTCGAGCTTAAGTGTAC	5880
Db	5821	ACGCGCTCTCTGACACGACCTCTCGACGACGGGAGCGCGAGATTCGAGCTTAAGTGTAC	5880

QY	5881	TCCTCCATGCCCCCCTTGAGGGGAGGCCGGGGATCCCGATCTGAGGAGGGCTTGG	5940
Db	5881	TCCTCCATGCCCCCCTTGAGGGGAGGCCGGGGATCCCGATCTGAGGAGGGCTTGG	5940
QY	5941	TCCTACCGTAAAGCGAGAGGCTAGTAGAGACGTGCTGCTCGATGTCCTACACATGG	6000
Db	5941	TCCTACCGTAAAGCGAGAGGCTAGTAGAGACGTGCTGCTCGATGTCCTACACATGG	6000
QY	6001	ACAGAGCCCGCTGATCAGCGCCATCGCTGGGAGGAGAAACCAACCTGCCCATATGACACTG	6060
Db	6001	ACAGAGCCCGCTGATCAGCGCCATCGCTGGGAGGAGAAACCAACCTGCCCATATGACACTG	6060
QY	6121	CTGGGGGAGAAAGAGTGCACCTTTGACAGAGCTGACAGTCTTGAGAGCAGCTACCGGAG	6180
Db	6121	CTGGGGGAGAAAGAGTGCACCTTTGACAGAGCTGACAGTCTTGAGAGCAGCTACCGGAG	6180
QY	6181	GTGCTCAAGGAGATGAAGGCGAAGGGCTGCACATTAAAGCTTAATCTGTATCCGTGGAG	6240
Db	6181	GTGCTCAAGGAGATGAAGGCGAAGGGCTGCACATTAAAGCTTAATCTGTATCCGTGGAG	6240
QY	6241	GAACCTGTAAAGCTGAGCGCCGCCACATTCGGGCAGATCTAAATTTGGCTATGGGGCAAG	6300
Db	6241	GAACCTGTAAAGCTGAGCGCCGCCACATTCGGGCAGATCTAAATTTGGCTATGGGGCAAG	6300
QY	6301	GACGTCCGGAACTATCCAGCAAGGCCGTTAACACATCCGTCGGTGTGAAGGACTTG	6360
Db	6301	GACGTCCGGAACTATCCAGCAAGGCCGTTAACACATCCGTCGGTGTGAAGGACTTG	6360
QY	6361	CTGGAAGACACTGAGCAGCAATTTGACACACCATCATGGCAAAAATAGAGTTTCTGCG	6420
Db	6361	CTGGAAGACACTGAGCAGCAATTTGACACACCATCATGGCAAAAATAGAGTTTCTGCG	6420
QY	6421	GTCCAACCCAGAAAGGGGGGCCGCAAGCCAGCTCCCTTATGTATTCCTCAGATTTGGG	6480
Db	6421	GTCCAACCCAGAAAGGGGGGCCGCAAGCCAGCTCCCTTATGTATTCCTCAGATTTGGG	6480
QY	6481	GTTGCTGTATGCGAGAAATAGGCCCTTTCAGATGTGTTCCACCTCCCTCAGGCGTG	6540
Db	6481	GTTGCTGTATGCGAGAAATAGGCCCTTTCAGATGTGTTCCACCTCCCTCAGGCGTG	6540
QY	6541	ATGGGCTTCCTCATACGATTCCTCAATACTCTCTCTGACACGGGCTGAGTTCTCGTGAAT	6600
Db	6541	ATGGGCTTCCTCATACGATTCCTCAATACTCTCTCTGACACGGGCTGAGTTCTCGTGAAT	6600
QY	6601	GCTCGGAAAGCGAAGAAATCCCTATAGGGCTTGCGATATGACACCCGCTGTTTGACGA	6660
Db	6601	GCTCGGAAAGCGAAGAAATCCCTATAGGGCTTGCGATATGACACCCGCTGTTTGACGA	6660
QY	6661	ACGGTCACTAGAAATGCAATCCGTTGTGAGAGATCAATACCATTGTTGACTTGGCC	6720
Db	6661	ACGGTCACTAGAAATGCAATCCGTTGTGAGAGATCAATACCATTGTTGACTTGGCC	6720
QY	6721	CCCGAAGCGACAGGCCCATTAAGTGGCTCACAGACGGCTTTACATCGGGGCCCCCTG	6780
Db	6721	CCCGAAGCGACAGGCCCATTAAGTGGCTCACAGACGGCTTTACATCGGGGCCCCCTG	6780
QY	6781	ACTAATTCTAAAGGGCGAGACTGGGCTATCGCCGCTGGCGGAGGGGTACTGAGC	6840
Db	6781	ACTAATTCTAAAGGGCGAGACTGGGCTATCGCCGCTGGCGGAGGGGTACTGAGC	6840
QY	6841	ACCAAGCTGGTAAATTACCTCTACATGTTACTTTGAAGGCGCGCTGTGAGACTCGC	6900
Db	6841	ACCAAGCTGGTAAATTACCTCTACATGTTACTTTGAAGGCGCGCTGTGAGACTCGC	6900
QY	6901	AAGCCCAAGGACTGACAGATGTCGTATGGGAGAGACCTTGTTATCTGTGAAGC	6960
Db	6901	AAGCCCAAGGACTGACAGATGTCGTATGGGAGAGACCTTGTTATCTGTGAAGC	6960
QY	6961	CGCGGAGCCCAAGGAGAGGCGAGCTTACGCGCCCTTACGAGGCTATGATGATGATAC	7020

Db	6961	GGGGGGACCCAAAGAGAGACGAGGGGACCTTACGSGCCTTACGAGAGGCTATGACTAGATAC	7020
QY	7021	TCCTGCCCCCTGGGGACCCGCCAAACGAATACGACTTGGAGTTGATATACATATGC	7080
Db	7021	TCCTGCCCCCTGGGGACCCGCCAAACGAATACGACTTGGAGTTGATATACATATGC	7080
QY	7081	TCCTGCATGAGTGAAGCGGACGACGATGCACTCGGCAAAAGGTTACTATATCCCGGT	7140
Db	7081	TCCTGCATGAGTGAAGCGGACGACGATGCACTCGGCAAAAGGTTACTATATCCCGGT	7140
QY	7141	GACCCCAACACCCCTTGGCGGGGCGTGCSTGGGAGAACGCTAGACACACTCCAGTCAT	7200
Db	7141	GACCCCAACACCCCTTGGCGGGGCGTGCSTGGGAGAACGCTAGACACACTCCAGTCAT	7200
QY	7201	TCCTGGCTAAGGCAACATCATCATGATATGCGCCACCCTTGTGGCAAGATGATCTCTGATG	7260
Db	7201	TCCTGGCTAAGGCAACATCATCATGATATGCGCCACCCTTGTGGCAAGATGATCTCTGATG	7260
QY	7261	ACCTATTTCTCTCCATCCTCTTCTAGCTCAGAGACACTTGAAAAAGCCCTAATTTGTAG	7320
Db	7261	ACCTATTTCTCTCCATCCTCTTCTAGCTCAGAGACACTTGAAAAAGCCCTAATTTGTAG	7320
QY	7321	ATCTACGGGGCCTGTACTCCATTTAGCGCACCTTGACCTACCTCAGATCTTACAGACTC	7380
Db	7321	ATCTACGGGGCCTGTACTCCATTTAGCGCACCTTGACCTACCTCAGATCTTACAGACTC	7380
QY	7381	CATGGCCCTTACGGCATTTTCACTCCATAGTACTTCCAGGAGAGTCAATAGGGTGGT	7440
Db	7381	CATGGCCCTTACGGCATTTTCACTCCATAGTACTTCCAGGAGAGTCAATAGGGTGGT	7440
QY	7441	TCATGCTCAGAAACTTGGGGATCGCGCCTTGCGAGTCTGAGACATCGSGCCAGAAGT	7500
Db	7441	TCATGCTCAGAAACTTGGGGATCGCGCCTTGCGAGTCTGAGAGACATCGSGCCAGAAGT	7500
QY	7501	GTCGGCGCTTAGCTACTGTCGCCAGGGGGAGGGGCTGCCACTGTGTGCAAGTACCTCTTC	7560
Db	7501	GTCGGCGCTTAGCTACTGTCGCCAGGGGGAGGGGCTGCCACTGTGTGCAAGTACCTCTTC	7560
QY	7561	AACGTGGCAGTAAAGGCCAAAGCTCAAACTCACTCCATCCCGGCTGCTCCACGTTGGAT	7620
Db	7561	AACGTGGCAGTAAAGGCCAAAGCTCAAACTCACTCCATCCCGGCTGCTCCACGTTGGAT	7620
QY	7621	TTATCCAGCTGTTGCTGTGCGGTAGAGCGGGGAGACATATATACAGCCTGTCTGCT	7680
Db	7621	TTATCCAGCTGTTGCTGTGCGGTAGAGCGGGGAGACATATATACAGCCTGTCTGCT	7680
QY	7681	GCCGAGCCCCGCTGTTCACTGATGTGCTACTCTCACTTCTGTAGGGGTAGGCATCTAT	7740
Db	7681	GCCGAGCCCCGCTGTTCACTGATGTGCTACTCTCACTTCTGTAGGGGTAGGCATCTAT	7740
QY	7741	CTACGCCCAACCCGATAGCGGGGACTTAACACTCCAGGCCAAATAGGCCATCTGTTTT	7800
Db	7741	CTACGCCCAACCCGATAGCGGGGACTTAACACTCCAGGCCAAATAGGCCATCTGTTTT	7800
QY	7801	TTTCCCTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTTT	7860
Db	7801	TTTCCCTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTTT	7860
QY	7861	TTTTTCCTTTTTTTTTCTTTTCTTTCTTTCCTTTGCTGAGCTCCATCTTAGCCCTAGTCAGGC	7920
Db	7861	TTTTTCCTTTTTTTTTCTTTTCTTTCTTTCCTTTGCTGAGCTCCATCTTAGCCCTAGTCAGGC	7920
QY	7921	TAGCGTAAAGGTCGCTGAGCGCCTTGATGTGAGAGAGGCTGATAGTGGGCTCTGCG	7980
Db	7921	TAGCGTAAAGGTCGCTGAGCGCCTTGATGTGAGAGAGGCTGATAGTGGGCTCTGCG	7980
QY	7981	AGATCAAGT 7989	
Db	7981	AGATCAAGT 7989	

RESULT 10

AA25321
ID AAD25321 standard; cDNA; 7987 BP.
XX
AC AAD25321;
XX
DT 12-MAR-2002 (first entry)
XX
DE Hepatitis C virus (HCV) replBartman/delta20's cDNA.
XX
KM Hepatitis C virus; HCV, transfection; infection; virus neutralisation;
KM gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
KM ss.
XX
OS Hepatitis C virus.
XX
PN MO200189364-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001MO-US16822.
XX
PR 23-MAY-2000; 2000US-0576989.
XX
PA (UNIM) UNIV WASHINGTON.
XX
PI Rice CM, Blight KJ;
XX
DR WPI; 2002-066755/09.
XX
PT Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences
PT
XX
PS Claim 44; Page 66-69; 174pp; English.
XX
CC The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets,
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficiency replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays,
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated HCV derivatives as possible vaccine candidates, engineering
CC of attenuated or defective HCV derivatives for expression of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) replBartman/delta20's cDNA.
XX
SQ Sequence 7987 BP; 1647 A; 2368 C; 2243 G; 1729 T; 0 other;

Query Match 99.7%; Score 7968.5; DB 24; Length 7987;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7983; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 1 GCCAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAGTACTG 60
|||||
|||||

DB 1 GCCAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAGTACTG 60
QY 1 TCTTCACGCGAAGAGCGCTTAGCCATGATGATGCTGCTGAGAGCCCTCCAGGAC 120
61 TCTTCACGCGAAGAGCGCTTAGCCATGATGATGCTGCTGAGAGCCCTCCAGGAC 120
DB 61 TCTTCACGCGAAGAGCGCTTAGCCATGATGATGCTGCTGAGAGCCCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAGAACCGGTGAGTACACCGGAATTCAG 180
121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAGAACCGGTGAGTACACCGGAATTCAG 180
DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAGAACCGGTGAGTACACCGGAATTCAG 180
QY 181 GACGACCGGCTCTTCTTGTGATTAACCCGCTCAATGCCCTGGAGATTGGGCGTCC 240
181 GACGACCGGCTCTTCTTGTGATTAACCCGCTCAATGCCCTGGAGATTGGGCGTCC 240
DB 181 GACGACCGGCTCTTCTTGTGATTAACCCGCTCAATGCCCTGGAGATTGGGCGTCC 240
QY 241 GCGAGACTGCTAGGCGGATGATGTTGAGTGCAGAAAGCCCTTGCTAGCTGCTATAG 300
241 GCGAGACTGCTAGGCGGATGATGTTGAGTGCAGAAAGCCCTTGCTAGCTGCTATAG 300
DB 241 GCGAGACTGCTAGGCGGATGATGTTGAGTGCAGAAAGCCCTTGCTAGCTGCTATAG 300
QY 301 GTGCTTGGAGTGGCCCGGAGAGTCTGTAGACCGGTGACACCATGAGCAGCAATCTTAAC 360
301 GTGCTTGGAGTGGCCCGGAGAGTCTGTAGACCGGTGACACCATGAGCAGCAATCTTAAC 360
DB 301 GTGCTTGGAGTGGCCCGGAGAGTCTGTAGACCGGTGACACCATGAGCAGCAATCTTAAC 360
QY 361 CTCAGAGAAACCAAGAGGGGCGCCATGATGACAGATGATGATGACAGAGTTGTC 420
361 CTCAGAGAAACCAAGAGGGGCGCCATGATGACAGATGATGATGACAGAGTTGTC 420
DB 361 CTCAGAGAAACCAAGAGGGGCGCCATGATGACAGATGATGATGACAGAGTTGTC 420
QY 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGAGCACAACAGACATCGCTGCT 480
421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGAGCACAACAGACATCGCTGCT 480
DB 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGAGCACAACAGACATCGCTGCT 480
QY 481 CTGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481 CTGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CTGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 ACTGTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
541 ACTGTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 ACTGTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
601 CGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 CGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 TGTATTGGGGGAGAGTGGCGGGGAGAGATCTCTGTATCTGCTGCTGCTGCTGCT 720
661 TGTATTGGGGGAGAGTGGCGGGGAGAGATCTCTGTATCTGCTGCTGCTGCTGCTGCT 720
DB 661 TGTATTGGGGGAGAGTGGCGGGGAGAGATCTCTGTATCTGCTGCTGCTGCTGCTGCT 720
QY 721 AAGTATCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721 AAGTATCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 AAGTATCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CATTGACACCAAGCGAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 840
781 CATTGACACCAAGCGAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 840
DB 781 CATTGACACCAAGCGAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 840
QY 841 TTGTGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
841 TTGTGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 841 TTGTGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 901 CCAGGCTCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
901 CCAGGCTCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CCAGGCTCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GCTTCGCGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
961 GCTTCGCGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 GCTTCGCGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 TGGGTGCGGAGCGCTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1080
1021 TGGGTGCGGAGCGCTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1080
DB 1021 TGGGTGCGGAGCGCTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1080
QY 1081 TTGGGCGGGAATGAGCTACCGCTTCTGCTGCTTACGATGCGCGCTCCGATTTGCG 1140
1081 TTGGGCGGGAATGAGCTACCGCTTCTGCTGCTTACGATGCGCGCTCCGATTTGCG 1140
DB 1081 TTGGGCGGGAATGAGCTACCGCTTCTGCTGCTTACGATGCGCGCTCCGATTTGCG 1140

D	3301	GCTGTGTAAGACCTCAGCCCGCGAGACCTCAGTTAGTTGGGGGCTTACCTAAACACA	3350
O	3361	CCAGGGTGGCCGCTGTGCCAGACCATCTGGAGTTCTGGAGAGCGCTTTACAGGCTC	3420
D	3361	CCAGGGTGGCCGCTGTGCCAGACCATCTGGAGTTCTGGAGAGCGCTTTACAGGCTC	3420
O	3421	ACCACATAGAGGCCCATTTCTGTCCAGACTAAGCAGGAGAGACAATTCCTCCATC	3480
D	3421	ACCACATAGAGGCCCATTTCTGTCCAGACTAAGCAGGAGAGACAATTCCTCCATC	3480
O	3481	CTGGTAGCATACAGAGCTACGGTGTGGCGCAGGGGCTCAGGCTCCACTCATCTGGAC	3540
D	3481	CTGGTAGCATACAGAGCTACGGTGTGGCGCAGGGGCTCAGGCTCCACTCATCTGGAC	3540
O	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGGCTACGGTGCACGGGCGCAAGCCCTCTG	3600
D	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGGCTACGGTGCACGGGCGCAAGCCCTCTG	3600
O	3601	TATAGGCGGGAGCCGTTCAAAAGAGGTTACTACACACACCCCATTAACCAATATATC	3660
D	3601	TATAGGCGGGAGCCGTTCAAAAGAGGTTACTACACACACCCCATTAACCAATATATC	3660
O	3661	ATGGCATCATGTGGGCTGACCTGAGGTCGTACGAGCACTGGTGTGTGTAGGGGA	3720
D	3661	ATGGCATCATGTGGGCTGACCTGAGGTCGTACGAGCACTGGTGTGTGTAGGGGA	3720
O	3721	GTCCAGAGAGTCTGGGCGGGTATTGGCTGCACACAGGCGGTGATTTGGGAGG	3780
D	3721	GTCCAGAGAGTCTGGGCGGGTATTGGCTGCACACAGGCGGTGATTTGGGAGG	3780
O	3781	ATCATCTTGTCCGGAAGCGCGGCATCTCCGACAGAGGAAGTCTTTACCGGGAGTTC	3840
D	3781	ATCATCTTGTCCGGAAGCGCGGCATCTCCGACAGAGGAAGTCTTTACCGGGAGTTC	3840
O	3841	GATGATGATGAAGATGTGGCTCACACCTCCATACATCCAGACGGGAATGAGAGCTGCC	3900
D	3841	GATGATGATGAAGATGTGGCTCACACCTCCATACATCCAGACGGGAATGAGAGCTGCC	3900
O	3901	GAAACATTCGGAAGAGGAGGATGGGTTGCTGCAAAAGAGCCACCAAGCAGAGGAGGCT	3960
D	3901	GAAACATTCGGAAGAGGAGGATGGGTTGCTGCAAAAGAGGAGGATGGGTTGCTGCAAAAGAGGAGGAGGCT	3960
O	3961	GCTGTCCCGGAGGGAATCCAAAGTGGGAGCCCTGGAAGCTTCGGGGAGAGCATATG	4020
D	3961	GCTGTCCCGGAGGGAATCCAAAGTGGGAGCCCTGGAAGCTTCGGGGAGAGCATATG	4020
O	4021	TGGAATTCATACAGCGGAGTACATATTTAGCAGGCTTGTCCACTGTGCTGGCAACCC	4080
D	4021	TGGAATTCATACAGCGGAGTACATATTTAGCAGGCTTGTCCACTGTGCTGGCAACCC	4080
O	4081	GGCATAGCATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4140
D	4081	GGCATAGCATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4140
O	4141	ACCCTCCTGTTTAAATCTCTGGGGGATGAGTGGCGCCCAACTGTCTCTCCAGAGCT	4200
D	4141	ACCCTCCTGTTTAAATCTCTGGGGGATGAGTGGCGCCCAACTGTCTCTCCAGAGCT	4200
O	4201	GCTTCTGTTTGAAGGAGCGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4260
D	4201	GCTTCTGTTTGAAGGAGCGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4260
O	4261	AAGTGTCTGTGATATTTTGGAGGATATGAGAGCAGAGGATGAGAGGAGGAGGAGGAG	4320
D	4261	AAGTGTCTGTGATATTTTGGAGGATATGAGAGCAGAGGATGAGAGGAGGAGGAGGAGGAG	4320
O	4321	TTTAAGGATGAGAGCGGAGGATGCTCCACGAGAGAGCTGGCTAACCTACTGCTGCT	4380
D	4321	TTTAAGGATGAGAGCGGAGGATGCTCCACGAGAGAGCTGGCTAACCTACTGCTGCT	4380
O	4381	ATCCTTCCCTGAGCCCTAGTGTGTGGGCTGTGTGCGCAACGATCTGCTGGGAC	4440
D	4381	ATCCTTCCCTGAGCCCTAGTGTGTGGGCTGTGTGCGCAACGATCTGCTGGGAC	4440
O	4441	GTGGGCCCAAGGAGGAGGAGGAGTGTGAGTGTGAGTGAACGAGCTGTGCTTCCGCGG	4500
D	4441	GTGGGCCCAAGGAGGAGGAGGAGTGTGAGTGTGAGTGAACGAGCTGTGCTTCCGCGG	4500
O	4501	GGTAACACAGTGTCCCGCCAGCAGTATGTGGCTGAGAGGAGGAGGAGGAGGAGGAGGAG	4560
D	4501	GGTAACACAGTGTCCCGCCAGCAGTATGTGGCTGAGAGGAGGAGGAGGAGGAGGAGGAG	4560
O	4561	CAGATCCTTCTAGTCTTACATCACTACGCTGTGAAAGAGGCTTCAACAGTGTATAC	4620
D	4561	CAGATCCTTCTAGTCTTACATCACTACGCTGTGAAAGAGGCTTCAACAGTGTATAC	4620
O	4621	GAGGAGTGTCCACGAGCAGTGTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4680
D	4621	GAGGAGTGTCCACGAGCAGTGTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4680
O	4681	ACGATGTGTAGTATTTAAGACCTGCTCCAGTCCAAAGCTCTCCGCAATTTGCCGGA	4740
D	4681	ACGATGTGTAGTATTTAAGACCTGCTCCAGTCCAAAGCTCTCCGCAATTTGCCGGA	4740
O	4741	GTCCCTTCTCTCATGTGTAAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4800
D	4741	GTCCCTTCTCTCATGTGTAAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4800
O	4801	CAAAACCTGCTCCATGTGAGACAGATCACCGGACATGTGAAAAGGTTCCATGAGG	4860
D	4801	CAAAACCTGCTCCATGTGAGACAGATCACCGGACATGTGAAAAGGTTCCATGAGG	4860
O	4861	ATCGTGGGAGCTAGAGACCTGTAGTAAACAGTGGCATGGAATTCCTTAAAGCGTAC	4920
D	4861	ATCGTGGGAGCTAGAGACCTGTAGTAAACAGTGGCATGGAATTCCTTAAAGCGTAC	4920
O	4921	ACCAGGAGGCTTGCAGCGCCCTCCCGGCGCAATTTCTTAAAGGCTGTGGCGGCTG	4980
D	4921	ACCAGGAGGCTTGCAGCGCCCTCCCGGCGCAATTTCTTAAAGGCTGTGGCGGCTG	4980
O	4981	GCTGTGAGAGTACGTGAGGATGTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5040
D	4981	GCTGTGAGAGTACGTGAGGATGTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5040
O	5041	ACCAGTCAACAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5100
D	5041	ACCAGTCAACAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5100
O	5101	GATGGAGTGGGCTTGCAGAGTACCTCAGAGTGCACAAACCCCTCTACAGGAGGAGGAGG	5160
D	5101	GATGGAGTGGGCTTGCAGAGTACCTCAGAGTGCACAAACCCCTCTACAGGAGGAGGAGG	5160
O	5161	ACATTCCTGTGGGCTCAATCAATACCTGGTGGGTCACAGGAGGAGGAGGAGGAGGAGGAG	5220
D	5161	ACATTCCTGTGGGCTCAATCAATACCTGGTGGGTCACAGGAGGAGGAGGAGGAGGAGGAG	5220
O	5221	CCGAGAGTACAGTGTCTCACTTCACTGCTCACGAGCCCTCCACATTTAC	


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QY 5521 AGGAAATATCCGTTCCGGCGAGATCTGCGGAGGATCCAGAAATTCCTCGAGCGATG 5580
DB 5521 AGGAAATATCCGTTCCGGCGAGATCTGCGGAGGATCCAGAAATTCCTCGAGCGATG 5580
QY 5581 CCCATATGCGACGCCCGGATTTACAAACCTCCACTGTAGATCTCGAAGACCGCGAC 5640
DB 5581 CCCATATGCGACGCCCGGATTTACAAACCTCCACTGTAGATCTCGAAGACCGCGAC 5640
QY 5641 TACATCCCTCCAGTGTACACGGGATGATCCAGTCCCGCCGCAAGGCGCCCTCCGATACCA 5700
DB 5641 TACATCCCTCCAGTGTACACGGGATGATCCAGTCCCGCCGCAAGGCGCCCTCCGATACCA 5700
QY 5701 CTTCCACGAGAGAGAGAGAGGATTTGTCGTGCAAGATCTACCGTGTCTTCTGCTTGGCG 5760
DB 5701 CTTCCACGAGAGAGAGAGAGGATTTGTCGTGCAAGATCTACCGTGTCTTCTGCTTGGCG 5760
QY 5761 GAGCTCGCCACAAAGACCTTCGCGACCTCCGAATGCTCGCGCGTGCAGACGCGGACGGCA 5820
DB 5761 GAGCTCGCCACAAAGACCTTCGCGACCTCCGAATGCTCGCGCGTGCAGACGCGGACGGCA 5820
QY 5821 ACGGCTCTCTCTGACACAGCCCTCCGACGAGCGGACGCGGATCCGAGCTTGAGTCTGAC 5880
DB 5821 ACGGCTCTCTCTGACACAGCCCTCCGACGAGCGGACGCGGATCCGAGCTTGAGTCTGAC 5880
QY 5881 TCTCCCAATGCCCCCTTTAGGGGGAGCCGGGGGATCCCGATCTCAGGAGCGGCTTGG 5940
DB 5881 TCTCCCAATGCCCCCTTTAGGGGGAGCCGGGGGATCCCGATCTCAGGAGCGGCTTGG 5940
QY 5941 TCTACCGTAAGCAGAGAGGATAGTGAAGAGCTGCTGCTGCTGATGCTACAGCATGG 6000
DB 5941 TCTACCGTAAGCAGAGAGGATAGTGAAGAGCTGCTGCTGCTGATGCTACAGCATGG 6000
QY 6001 ACGGGGCGCTGATCACCGCATGCGTGGGAGAGAAACCAACTCCCATCATCTACTG 6060
DB 6001 ACGGGGCGCTGATCACCGCATGCGTGGGAGAGAAACCAACTCCCATCATCTACTG 6060
QY 6061 AGCAACTCTTGTGCTCGTACACCAACTTGTGTATGTACTACAACTCTCGAGCGCAAGC 6120
DB 6061 AGCAACTCTTGTGCTCGTACACCAACTTGTGTATGTACTACAACTCTCGAGCGCAAGC 6120
QY 6121 CTGGGCGAGAGAGGATGCACTTGTGACAGATGCGAGTCCGAGACGACACTACCGGAC 6180
DB 6121 CTGGGCGAGAGAGGATGCACTTGTGACAGATGCGAGTCCGAGACGACACTACCGGAC 6180
QY 6181 GTGCTCAAGSAGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAACTCTATCCGTGAG 6240
DB 6181 GTGCTCAAGSAGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAACTCTATCCGTGAG 6240
QY 6241 GAAGCCTGTAGCTGACGCCGCCCACTTTGGCCAGATCTAAATTTGGCTATGGGCAAG 6300
DB 6241 GAAGCCTGTAGCTGACGCCGCCCACTTTGGCCAGATCTAAATTTGGCTATGGGCAAG 6300
QY 6301 GACGTCGGAACCTATCCAGCAAGGCGGTTAACCAACATCGGTCGCTGGAAGGACTG 6360
DB 6301 GACGTCGGAACCTATCCAGCAAGGCGGTTAACCAACATCGGTCGCTGGAAGGACTG 6360
QY 6361 CTGAGAGACACTGAGACACCAATTTGACACCAACCATATGGCAAAAATGAGGTTTCTGC 6420
DB 6361 CTGAGAGACACTGAGACACCAATTTGACACCAACCATATGGCAAAAATGAGGTTTCTGC 6420
QY 6421 GTCCAAACAGAGAGAGGGGGGCGCAAGCCAGCTGCGCTATGCTATTCAGATTTGGG 6480
DB 6421 GTCCAAACAGAGAGAGGGGGGCGCAAGCCAGCTGCGCTATGCTATTCAGATTTGGG 6480
QY 6481 GTTCGTGTGTGCGAGAAAATGGCCTTTAGATGTGTGTCTCCACCTCTCCAGGCGGTG 6540
DB 6481 GTTCGTGTGTGCGAGAAAATGGCCTTTAGATGTGTGTCTCCACCTCTCCAGGCGGTG 6540
QY 6541 ATGGGCTCTTCATAGGATTTCAATATCTCTCTGAGACAGCGGGTGTGAGTCTCTGTGAT 6600
DB 6541 ATGGGCTCTTCATAGGATTTCAATATCTCTCTGAGACAGCGGGTGTGAGTCTCTGTGAT 6600
QY 6601 GCCGGAAGCAGAGAAATGCCCTATGSGCTTCGATATGACACCCGCTTTGACTCA 6660
DB 6601 GCCGGAAGCAGAGAAATGCCCTATGSGCTTCGATATGACACCCGCTTTGACTCA 6660
QY 6661 ACGGTACTAGAGATGACATCCGTTGAGAGAGTCAATCTACCAATGTTGTGACTGGCC 6720
DB 6661 ACGGTACTAGAGATGACATCCGTTGAGAGAGTCAATCTACCAATGTTGTGACTGGCC 6720
QY 6721 CCCGAAGCCGACAGGCCATTAAGGTGCGACAGAGCGGCTTACATGGGGGGCCCTG 6780
DB 6721 CCCGAAGCCGACAGGCCATTAAGGTGCGACAGAGCGGCTTACATGGGGGGCCCTG 6780
QY 6781 ACTAATTTCTAAAGGCGAGACTGCGGCTATGCGCGGTGCGCGGAGCGGCTGACTGACG 6840
DB 6781 ACTAATTTCTAAAGGCGAGAACTGCGGCTATGCGCGGTGCGCGGAGCGGCTGACTGACG 6840
QY 6841 ACCAGCTGCGGTAATACCTTCACATGTTACTTGAAGCGCGCTGCGGCTGTGAGACTGCG 6900
DB 6841 ACCAGCTGCGGTAATACCTTCACATGTTACTTGAAGCGCGCTGCGGCTGTGAGACTGCG 6900
QY 6901 AAGCTCCAGAGACTGACAGATGCTGATGCGAGAGACGACCTTGTGTTATCTGTAAGC 6960
DB 6901 AAGCTCCAGAGACTGACAGATGCTGATGCGAGAGACGACCTTGTGTTATCTGTAAGC 6960
QY 6961 GCGGGACCCCAAGAGACGAGCGAGCCCTACGCGCTTACAGGAGCTATGACTAGATAC 7020
DB 6961 GCGGGACCCCAAGAGAGACGAGCGAGCCCTACGCGCTTACAGGAGCTATGACTAGATAC 7020
QY 7021 TCTGCCCCCTGSGGAGCCGCGCAACAGAAATACGACTTGAATGATTAACATCATGC 7080
DB 7021 TCTGCCCCCTGSGGAGCCGCGCAACAGAAATACGACTTGAATGATTAACATCATGC 7080
QY 7081 TCTCTCAATGTGTCAATGCTCGGACGATGCTATGCGAAAAGGTTACTATCTACCCGT 7140
DB 7081 TCTCTCAATGTGTCAATGCTCGGACGATGCTATGCGAAAAGGTTACTATCTACCCGT 7140
QY 7141 GACCCACACACCCCGCTTGCAGGCGTGTGCTGGAGACAGCTAGACACCTCCAGTCAAT 7200
DB 7141 GACCCACACACCCCGCTTGCAGGCGTGTGCTGGAGACAGCTAGACACCTCCAGTCAAT 7200
QY 7201 TCTGAGCTAGAGACATCATATGTATGCGCCACTTGTGGGCAAGATATCTGATG 7260
DB 7201 TCTGAGCTAGAGACATCATATGTATGCGCCACTTGTGGGCAAGATATCTGATG 7260
QY 7261 ACTCATTTTCTTCCATCCCTTCTAGTCAAGACAACTTGAAAAAGCCCTAGATTGTAG 7320
DB 7261 ACTCATTTTCTTCCATCCCTTCTAGTCAAGACAACTTGAAAAAGCCCTAGATTGTAG 7320
QY 7321 ATCTACGGGCGCTGTACTCATTTAGCCACTTGAACCTACCTCAGATCATTCAGACATC 7380
DB 7321 ATCTACGGGCGCTGTACTCATTTAGCCACTTGAACCTACCTCAGATCATTCAGACATC 7380
QY 7381 CATGGGCTTAGGCACTTTTCACTCATATGTTACTTCCAGGAGATCAATAGGATGCT 7440
DB 7381 CATGGGCTTAGGCACTTTTCACTCATATGTTACTTCCAGGAGATCAATAGGATGCT 7440
QY 7441 TCAATGCTTAGGAACTTGGGATACCGGCTTGCAGTGTGAGACATCGGCGCAAGAT 7500
DB 7441 TCAATGCTTAGGAACTTGGGATACCGGCTTGCAGTGTGAGACATCGGCGCAAGAT 7500
QY 7501 GTCCGCGTAGGCTACTGTCCAGGAGGAGGATGCTGACCTGAGGAGATTAATCTCTTC 7560
DB 7501 GTCCGCGTAGGCTACTGTCCAGGAGGAGGATGCTGACCTGAGGAGATTAATCTCTTC 7560
QY 7561 AACTGGGAGTAGAGACAACTCAAACTCACTCCATCCGCGCTGCTCCAGTGGAT 7620
DB 7561 AACTGGGAGTAGAGACAACTCAAACTCACTCCATCCGCGCTGCTCCAGTGGAT 7620
QY 7621 TTAATCAGAGGTTGTTCTGTTACAGCGGAGGAGACATATATACAGCTGTGCTGCT 7680
DB 7621 TTAATCAGAGGTTGTTCTGTTACAGCGGAGGAGACATATATACAGCTGTGCTGCT 7680
QY 7681 GCCGAGCCCGGCTGTTATGTGTGCTTACTCTTCTGTAGGGGTAGGACATCAT 7740
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Db	7681	GCCGACCCCGCTGCTTCATGTGAGCCTACTCTACTTCTGTGAGGGGAGGACATCTAT	7740
Oy	7741	CTACTCCCGACCGATGAGACGGGGAGCAATACACTCCAGCCCAATGAGCCATCTGT	7800
Db	7741	CTACTCCCGACCGATGAGACGGGGAGCAATACACTCCAGCCCAATGAGCCATCTGT	7800
Oy	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7858
Oy	7861	TTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	7859	TTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7918
Oy	7921	TAGCTGTGAAGAGTCCGTCAGCCGCTTGACTGCAGAGAGTGCATGACTAGGCTCTG	7980
Db	7919	TAGCTGTGAAGAGTCCGTCAGCCGCTTGACTGCAGAGAGTGCATGACTAGGCTCTG	7978
Oy	7981	AGATCAAGT 7989	
Db	7979	AGATCAAGT 7987	
RESULT 11			
ID	AAD25329	standard; CDNA: 7987 BP.	
AC	AAD25329;		
XX			
XX	12-MAR-2002 (first entry)		
DE	Hepatitis C virus (HCV) adaptive replicon VII cDNA.		
XX			
KM	Hepatitis C virus; HCV; transfection; infection; virus neutralisation;		
KW	gene therapy; vaccines; immunoprotection; hepatotropic; virucide; liver;		
KW	adaptive replicon VII; ss.		
OS	Hepatitis C virus.		
XX			
XX	W0200189364-A2.		
PD	29-NOV-2001.		
XX			
XX	23-MAY-2001; 2001WO-US16822.		
PF			
XX	23-MAY-2000; 2000US-0576989.		
PR			
FA	(UNIV) UNIV WASHINGTON.		
XX			
PI	Rice CM, Blight KJ;		
XX			
DR	WPI; 2002-066755/09.		
XX			
PT	Hepatitis C virus variants having greater transfection efficiency and		
PT	ability to survive subpassage, useful as a vaccine for immunizing		
PT	primate to the virus, comprise non-naturally occurring viral sequences		
XX			
PS	Disclosure; Page 84-87; 174pp; English.		
CC	The invention relates to Hepatitis C virus (HCV) variants which include		
CC	polynucleotides comprising non-naturally occurring HCV sequence and HCV		
CC	variants that have a transfection efficiency and ability to survive		
CC	subpassage greater than HCV that have wild-type polypeptide coding		
CC	regions. The polynucleotides of the invention are useful for identifying		
CC	a cell line that is permissive for infection with HCV and detecting		
CC	replication of HCV in cells of the cell line. They are also useful for		
CC	testing a compound for anti-viral properties and for inhibiting HCV		
CC	infection. They are also useful for the generation of defined HCV virus		
CC	stocks to develop in vitro and in vivo assays for virus neutralisation,		
CC	attachment, penetration and entry, structure/function studies on HCV		
CC	proteins and RNA elements and identification of new antiviral targets.		

Query Match	Best Local Similarity	99.7%	Score 7967	DB 24	Length 7987
Matches 7987	Conservative	0	Mismatches	5	Indels 2
			Gaps	1	
CC	a systematic survey of cell culture systems and conditions to identify				
CC	those that support wild-type and variant HCV RNA replication and				
CC	particle release, production of adaptive HCV variants capable of more				
CC	efficiently replication in cell culture, production of HCV variants with				
CC	altered tissue or species tropism, establishment of alternative animal				
CC	models for inhibitor evaluation including those supporting HCV variant				
CC	replication, development of cell-free HCV replication assays,				
CC	production of immunogenic HCV particles for vaccination, engineering of				
CC	attenuated HCV derivatives as possible vaccine candidates, engineering of				
CC	heterologous gene products for gene therapy and vaccine applications				
CC	and for utilisation of the HCV glycoproteins for targeted delivery of				
CC	therapeutic agents to the liver or other cell types with appropriate				
CC	receptors. Vaccine comprising these sequences is useful for inducing				
CC	immunoprotection to HCV in a primate. The present sequence is				
CC	Hepatitis C virus (HCV) adaptive replicon VII cDNA.				
XX					
SO	Sequence 7987 BP; 1647 A; 2368 C; 2242 G; 1730 T; 0 other:				
QY	1 GCGAGCCCCCGATTGGGGGCGACACTCCACATCACTACCTCCCTGTAGAACTACTG				
DB	1 GCGAGCCCCCGATTGGGGGCGACACTCCACATCACTACCTCCCTGTAGAACTACTG				
QY	61 TCTTTCAGCGAAGAAAGGCTAGCCATGAGCTAGTATGATGTTGTGACCTCCAGAC				
DB	61 TCTTTCAGCGAAGAAAGGCTAGCCATGAGCTAGTATGATGATGTTGTGACCTCCAGAC				
QY	121 CCCCCCTCCCGGAGAGACCATTAGTGGTGGGGAACCGGTAGTACACCGGAATTCACG				
DB	121 CCCCCCTCCCGGAGAGACCATTAGTGGTGGGGAACCGGTAGTACACCGGAATTCACG				
QY	121 CCCCCCTCCCGGAGAGACCATTAGTGGTGGGGAACCGGTAGTACACCGGAATTCACG				
DB	121 CCCCCCTCCCGGAGAGACCATTAGTGGTGGGGAACCGGTAGTACACCGGAATTCACG				
QY	181 GAGACCGGGTCTTCTTCTTGATCAACCGCTCAATGCTGTGAGATTGGGGTGGCCCC				
DB	181 GAGACCGGGTCTTCTTCTTGATCAACCGCTCAATGCTGTGAGATTGGGGTGGCCCC				
QY	241 GCGAGACTGTACCGCAGTAGTGTGGTTCGGGAAAGGCTTGTGGTACGCTGTATAG				
DB	241 GCGAGACTGTACCGCAGTAGTGTGGTTCGGGAAAGGCTTGTGGTACGCTGTATAG				
QY	301 GTGTTCGCGAGTCCCGGGAGGCTGTCTGTAAACCGTGCACATAGACAAATTCCTAAC				
DB	301 GTGTTCGCGAGTCCCGGGAGGCTGTCTGTAAACCGTGCACATAGACAAATTCCTAAC				
QY	361 CTCGAAGAAACCAAGAGGCGCGCATGATGATGAACAAAGATGATTCACAGAGTTCTC				
DB	361 CTCGAAGAAACCAAGAGGCGCGCATGATGATGAACAAAGATGATGATTCACAGAGTTCTC				
QY	421 CGGCGCTTGGGTGAGAGCGCTATTCGGCTATGACTGGGCAACAGACAAATGGCTGCT				
DB	421 CGGCGCTTGGGTGAGAGCGCTATTCGGCTATGACTGGGCAACAGACAAATGGCTGCT				
QY	481 CTGATGCGCGCTGTCTCCGCTGTCAAGGCGAGGGCGCGGCTCTTTTGTCAAGACG				
DB	481 CTGATGCGCGCTGTCTCCGCTGTCAAGGCGAGGGCGCGGCTCTTTTGTCAAGACG				
QY	541 ACGCTTCGGGTGCGCGTGAATGAACTGCAAGCAAGGACGAGGCGGCTATTCGTGGCTGGCA				
DB	541 ACGCTTCGGGTGCGCGTGAATGAACTGCAAGCAAGGACGAGGCGGCTATTCGTGGCTGGCA				
QY	601 CGAGGGCGCTTCTCTTCCGCGAGCTGTCTGCAAGTGTTCACCTGAAGCGGAAGGACTGCG				
DB	601 CGAGGGCGCTTCTCTTCCGCGAGCTGTCTGCAAGTGTTCACCTGAAGCGGAAGGACTGCG				
QY	661 TGCATTATGGGCGAAGTGCAGGGGCGAGATTCCTGTATCTACCTTGGCTCCGCGAGA				
DB	661 TGCATTATGGGCGAAGTGCAGGGGCGAGATTCCTGTATCTACCTTGGCTCCGCGAGA				
QY	721 AAGTATCATCATGCGTGAATGCGAGTGGGCGCTGATACCTTGATCCGGTACCTGCC				
DB	721 AAGTATCATCATGCGTGAATGCGAGTGGGCGCTGATACCTTGATCCGGTACCTGCC				

Db 721 AAGTATCCATCATGCGTGAATGCGCGGCTGATACGCTTGATCCGGCTACCTGCC 780
QY 781 CATTCGACCAACAGGAAATCGCATGACGACGACGACTCGATGAGAACCGGTC 840
Db 781 CATTCGACCAACAGGAAATCGCATGAGCGACGACGACTCGATGAGAACCGGTC 840
QY 841 TTGTGATGAGTGTGAGCAAGAGCATCAGGGGCTGGCGCAGCGCAATGTTG 900
Db 841 TTGTGATGAGTGTGAGCAAGAGCATCAGGGGCTGGCGCAGCGCAATGTTG 900
QY 901 CCAGGCTCAAGCGCGCATGCCGACGCGAGATCTGCTGTAACCATGGCGATGCT 960
Db 901 CCAGGCTCAAGCGCGCATGCCGACGCGAGATCTGCTGTAACCATGGCGATGCT 960
QY 961 GCTTGGCGAATTCATGAGTGAATGGCGCTTTCTGAGTATGATGAGTGGCGG 1020
Db 961 GCTTGGCGAATTCATGAGTGAATGGCGCTTTCTGAGTATGATGAGTGGCGG 1020
QY 1021 TGGGTGTGGCGAGCGCATATCAGACATAGCGTTGGTACCCGATATTGCTGAAGC 1080
Db 1021 TGGGTGTGGCGAGCGCATATCAGACATAGCGTTGGTACCCGATATTGCTGAAGC 1080
QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTGCTGCTTACGATGCGCGCTCCGATTCG 1140
Db 1081 TTGGCGGCAATGGGCTGACCGCTTCTGCTGCTTACGATGCGCGCTCCGATTCG 1140
QY 1141 AAGGATCGCCTTCTATCGCTTCTTACGAGTCTTCTGAGTTTAAACAGACACAGC 1200
Db 1141 AAGGATCGCCTTCTATCGCTTCTTACGAGTCTTCTGAGTTTAAACAGACACAGC 1200
QY 1201 GTTTCCTTACGCGGATATTCGCGCCCTCTCCCTCCCGCCCTACGTTACTGCG 1260
Db 1201 GTTTCCTTACGCGGATATTCGCGCCCTCTCCCTCCCGCCCTACGTTACTGCG 1260
QY 1261 CGAAGCGCTTGAATAGCGCGGTGTGTGTATGATTTATTTCCACCATATG 1320
Db 1261 CGAAGCGCTTGAATAGCGCGGTGTGTGTATGATTTATTTCCACCATATG 1320
QY 1321 CGCTTTTGGCAATGTAGGGCCCGGAACTGGCCCTGCTTCTTGAACAGATTCCT 1380
Db 1321 CGCTTTTGGCAATGTAGGGCCCGGAACTGGCCCTGCTTCTTGAACAGATTCCT 1380
QY 1381 AAGGATCTTCCCTCTCGCCAAAGAAATGCAAGGTCTGTGATGTCGTGAAGAA 1440
Db 1381 AAGGATCTTCCCTCTCGCCAAAGAAATGCAAGGTCTGTGATGTCGTGAAGAA 1440
QY 1441 GTTCTCTGAGAGCTTCTGAAGACAAACAGCTGTAGGACCTTTGAGGACGG 1500
Db 1441 GTTCTCTGAGAGCTTCTGAAGACAAACAGCTGTAGGACCTTTGAGGACGG 1500
QY 1501 AACCCCCCACTGGCGACAGGTGCTGTGCGGCAAAAGCAAGCTGTATAGATAC 1560
Db 1501 AACCCCCCACTGGCGACAGGTGCTGTGCGGCAAAAGCAAGCTGTATAGATAC 1560
QY 1561 GCAAGGCGGACACACCCAGTGCAGCTGTGAGTTGAGTATGTTGAGAAAGTCAA 1620
Db 1561 GCAAGGCGGACACACCCAGTGCAGCTGTGAGTTGAGTATGTTGAGAAAGTCAA 1620
QY 1621 TGGCTCTCTCAAGGCTATTAACAAGGGGCTGAAGGATGCCCAAGATGCCCAT 1680
Db 1621 TGGCTCTCTCAAGGCTATTAACAAGGGGCTGAAGGATGCCCAAGATGCCCAT 1680
QY 1681 ATGGGATCTGATCTGGGGCTCGGTGCACATCTTTACATGTGTTTAAAGGTTAAA 1740
Db 1681 ATGGGATCTGATCTGGGGCTCGGTGCACATCTTTACATGTGTTTAAAGGTTAAA 1740
QY 1741 AAGGTCAAGGCCCCGGAACAAGGGGAGTGTGTTCTTGAAGAAACAGATATACC 1800
Db 1741 AAGGTCAAGGCCCCGGAACAAGGGGAGTGTGTTCTTGAAGAAACAGATATACC 1800
QY 1801 ATGGCGCTATTACGGCTACTTCCAAAGACGAGGCGTACTTGCTGATCATCTACT 1860
Db 1801 ATGGCGCTATTACGGCTACTTCCAAAGACGAGGCGTACTTGCTGATCATCTACT 1860

QY 1861 AACCTCACAGGCGGGAGAGAGACAGTGCAGGGGAGGTCCAGGTGCTCCACCGCA 1920
Db 1861 AACCTCACAGGCGGGAGAGAGACAGTGCAGGGGAGGTCCAGGTGCTCCACCGCA 1920
QY 1921 ACACATCTTCTTGGCAGCTGCGTCAATGAGGCTGTGAGTGTCTATCATGTTG 1980
Db 1921 ACACATCTTCTTGGCAGCTGCGTCAATGAGGCTGTGAGTGTCTATCATGTTG 1980
QY 1981 GCTCAAGACCTTGGCGGCCCAAGGGCCCAATCACCAATGTACACCATGTGAC 2040
Db 1981 GCTCAAGACCTTGGCGGCCCAAGGGCCCAATCACCAATGTACACCATGTGAC 2040
QY 2041 CAGGACCTGTGAGTGGCAAGCGGCCCGGGGCGGTCTTGAACCATGACCTGC 2100
Db 2041 CAGGACCTGTGAGTGGCAAGCGGCCCGGGGCGGTCTTGAACCATGACCTGC 2100
QY 2101 GGCAGCTCGACCTTACTTGTGTCAGAGGATCCGATGTATTCGGTCCGCGG 2160
Db 2101 GGCAGCTCGACCTTACTTGTGTCAGAGGATCCGATGTATTCGGTCCGCGG 2160
QY 2161 GGGCAGAGGAGGGGAGCTTCTCCCGCAGGCGCGTCTTGAAGGGCTTTG 2220
Db 2161 GGGCAGAGGAGGGGAGCTTCTCCCGCAGGCGCGTCTTGAAGGGCTTTG 2220
QY 2221 GGGGCTCAGTGTCTGCGCCCTCGGGGACGCTGTGGCATCTTTCGGGCTGCTG 2280
Db 2221 GGGGCTCAGTGTCTGCGCCCTCGGGGACGCTGTGGCATCTTTCGGGCTGCTG 2280
QY 2281 ACCCGAGGGGTGCGAAGGCGTGTGACTTTACCCGTCGAGTGTATGAAACCATAG 2340
Db 2281 ACCCGAGGGGTGCGAAGGCGTGTGACTTTACCCGTCGAGTGTATGAAACCATAG 2340
QY 2341 CGGTCCCGGCTTTCAGGACAACTGCTCCCTCGGCGGATCCGACAGATTCAG 2400
Db 2341 CGGTCCCGGCTTTCAGGACAACTGCTCCCTCGGCGGATCCGACAGATTCAG 2400
QY 2401 GGCATCTACAGGCGCTTACGTGAGGGCAAGAGCATAGAGTCCGGCTGCTATGCA 2460
Db 2401 GGCATCTACAGGCGCTTACGTGAGGGCAAGAGCATAGAGTCCGGCTGCTATGCA 2460
QY 2461 GCCAAGGGTATAGGTGCTTCTGTAAGCCGCTGCGCGCACCTTATGTTGGG 2520
Db 2461 GCCAAGGGTATAGGTGCTTCTGTAAGCCGCTGCGCGCACCTTATGTTGGG 2520
QY 2521 GGTATATGTCTAAGGACATGTATCGAACCTTAACATCAGACGGGATAGACCATC 2580
Db 2521 GGTATATGTCTAAGGACATGTATCGAACCTTAACATCAGACGGGATAGACCATC 2580
QY 2581 ACCACGGGTGCCCCCATACGTAAGTCACTATAGCAAGTCTTTCGCGAGGTGTG 2640
Db 2581 ACCACGGGTGCCCCCATACGTAAGTCACTATAGCAAGTCTTTCGCGAGGTGTG 2640
QY 2641 TCTGGGGGCGCTATGACATCATATATGTATGATGATGCCCTAACATGATCA 2700
Db 2641 TCTGGGGGCGCTATGACATCATATATGTATGATGATGCCCTAACATGATCA 2700
QY 2701 ATCTGTGAGTGGCAAGTCTGTGACCAAGCGAGAGTGTGAGCGGCACTGTG 2760
Db 2701 ATCTGTGAGTGGCAAGTCTGTGACCAAGCGAGAGTGTGAGCGGCACTGTG 2760
QY 2761 CTGCGCACCGCTACGCTTCGCGGATCGGTCAACCGTGCACATCCAAACATGA 2820
Db 2761 CTGCGCACCGCTACGCTTCGCGGATCGGTCAACCGTGCACATCCAAACATGA 2820
QY 2821 GCTCTGTCCAGACTGAGAAATCCCTTTTATGCAAGGCAATCCCATGAGACCATC 2880
Db 2821 GCTCTGTCCAGACTGAGAAATCCCTTTTATGCAAGGCAATCCCATGAGACCATC 2880
QY 2881 AAGGGGGGAGGACCTCTATTTTGTGCCATTCAGAAAGAAATGTATGAGTGTGCG 2940
Db 2881 AAGGGGGGAGGACCTCTATTTTGTGCCATTCAGAAAGAAATGTATGAGTGTGCG 2940

QY	2941	AAAGTGTCCGGCCCTCGAGACTCAATGCTGTAGCATATATACCGGGGCTTGATGTATCCGTC	3000
Db	2941	AAAGTGTCCGGCCCTCGAGACTCAATGCTGTAGCATATATACCGGGGCTTGATGTATCCGTC	3000
QY	3001	ATACCACTAGCGGAGAGCGTCATTGTCTGAGGACAGGAGCGCTCTATATACGGGCTTTAC	3060
Db	3001	ATACCACTAGCGGAGAGCGTCATTGTCTGAGGAGAGGAGCGCTCTATATACGGGCTTTAC	3060
QY	3061	GGCGATTTCCAGCTCAGATTCAGATCTGCATACATGTGTACCCAGACAGTGCATTTACG	3120
Db	3061	GGCGATTTCCAGCTCAGATTCAGATCTGCATACATGTGTACCCAGACAGTGCATTTACG	3120
QY	3121	CTGAGCCGAGACCTTCACACATTGAGAGAGAGACCGTGTCCACAAGACGCGGTGTACGCTG	3180
Db	3121	CTGAGCCGAGACCTTCACACATTGAGAGAGAGACCGTGTCCACAAGACGCGGTGTACGCTG	3180
QY	3181	CAGCGGCGAGGACAGACTGCTAGGGGACAGATGGGCGATTACAGTTTGTATACCCAGGA	3240
Db	3181	CAGCGGCGAGGACAGACTGCTAGGGGACAGATGGGCGATTACAGTTTGTATACCCAGGA	3240
QY	3241	GAAAGGCGCCCTGGGCGATGTTCGATTCTCGGTTCTGTGCGATGCTATGACGCGGCGCTG	3300
Db	3241	GAAAGGCGCCCTGGGCGATGTTCGATTCTCGGTTCTGTGCGATGCTATGACGCGGCGCTG	3300
QY	3301	GCTTGTGTACGAGCTCACGCCCCCGGAGACCTCAGTTAGTTCCGGGCTTACTTAACACA	3360
Db	3301	GCTTGTGTACGAGCTCACGCCCCCGGAGACCTCAGTTAGTTCCGGGCTTACTTAACACA	3360
QY	3361	CCAGGTTGCCCTGTCTCCAGAGACCATCTGGAATTTGTGGAAGCGGTCTTTACAGGCGCTC	3420
Db	3361	CCAGGTTGCCCTGTCTCCAGAGACCATCTGGAATTTGTGGAAGCGGTCTTTACAGGCGCTC	3420
QY	3421	ACCCACTATAGAGCGCCCATTTCTGTCTCCAGACTAACAAGACGAGAGACAATCTCCCTAC	3480
Db	3421	ACCCACTATAGAGCGCCCATTTCTGTCTCCAGACTAACAAGACGAGAGACAATCTCCCTAC	3480
QY	3481	CTGTGTAGCATACCAAGGCTACGAGTGTGCGGCGAGGCTCAGAGCTCCACCTCATCTGTGGAG	3540
Db	3481	CTGTGTAGCATACCAAGGCTACGAGTGTGCGGCGAGGCTCAGAGCTCCACCTCATCTGTGGAG	3540
QY	3541	CAATGTGAGAGTCTCTCATACGGCTTAAGGCTACAGGCTGACAGGGGCAAGGCGCCCTGTG	3600
Db	3541	CAATGTGAGAGTCTCTCATACGGCTTAAGGCTACAGGCTGACAGGGGCAAGGCGCCCTGTG	3600
QY	3601	TATAGCGTGGAGCGCGTTCAAAAAGAGGTACTTACACACACCCCATTAACCAATATATC	3660
Db	3601	TATAGCGTGGAGCGCGCGTTCAAAAAGAGGTACTTACACACACCCCATTAACCAATATATC	3660
QY	3661	ATGGCATCATGTGGGCTGAGCCTGGAAGTGTGTACAGAGACCTGGGTGTGTTAGGCGGA	3720
Db	3661	ATGGCATCATGTGGGCTGAGCCTGGAAGTGTGTACAGAGACCTGGGTGTGTTAGGCGGA	3720
QY	3721	GTCCTAGCAGCTGTGCGCGCGGTATGTGCTGTACACAGGCGAGCGTGTATGTGTGGCAGG	3780
Db	3721	GTCCTAGCAGCTGTGCGCGCGGTATGTGCTGTACACAGGCGAGCGTGTATGTGTGGCAGG	3780
QY	3781	ATCATCTGTGTCCGGAAGACGCGGCATATTCCCGAAGGGAAGTCTTTACCGGAGGTTC	3840
Db	3781	ATCATCTGTGTCCGGAAGACGCGGCATATTCCCGAAGGGAAGTCTTTACCGGAGGTTC	3840
QY	3841	GATGAGATGGAAGAGTGGGCTCACACCTCCCTTACATGTGAACAGGGAATGTAGTGGCC	3900
Db	3841	GATGAGATGGAAGAGTGGGCTCACACCTCCCTTACATGTGAACAGGGAATGTAGTGGCC	3900
QY	3901	GATCAATTCAAACAGAAAGGCGCATGTGGGTTCTGTCAACACAGCACAAAGCAACGAGAGCT	3960
Db	3901	GATCAATTCAAACAGAAAGGCGCATGTGGGTTCTGTCAACACAGCACAAAGCAACGAGAGCT	3960
QY	3961	GCTGCTCCCGTGTGTGAATTCAGTGGCGGACCTCTGAAAGCTTCTGGGCGGAAGATATG	4020
Db	3961	GCTGCTCCCGTGTGTGAATTCAGTGGCGGACCTCTGAAAGCTTCTGGGCGGAAGATATG	4020
QY	4021	TGGAATTTTCATCAGCGGATACATATATTAGCAGGCTGTTCACCTGTGCTGTGCACACC	4080

Db	4021	TGGAATTCATACACCGGGATACAAATTTTAAAGACGCTGTCCACTCTGCTTGGACACCCC	4080
Qy	4081	GGCATACCATCATCGATGAGGCAATTCACAGCCTCATACCAAGCCGCTACCAACCCAAAT	4140
Db	4081	GGCATACCATCATCGATGAGGCAATTCACAGCCTCATACCAAGCCGCTACCAACCCAAAT	4140
Qy	4141	ACCCCTCGTATTAAATCTCTGGGGGGGATGGGATGGCCGCCCAACTTGTCTCTCCAGCCT	4200
Db	4141	ACCCCTCGTATTAAATCTCTGGGGGGGATGGGATGGCCGCCCAACTTGTCTCTCCAGCCT	4200
Qy	4201	GCTTCTGCTTTCGTAGGCGCCGCAATCGCTGGAGCGGCTGTGGCAGCATAGCCTTGGG	4260
Db	4201	GCTTCTGCTTTCGTAGGCGCCGCAATCGCTGGAGCGGCTGTGGCAGCATAGCCTTGGG	4260
Qy	4261	AAGGTGCTGTGGATATTATTGGCAGGATATATGAGCAGGGGATGGACAGCGCGCTGTGGCC	4320
Db	4261	AAGGTGCTGTGGATATTATTGGCAGGATATATGAGCAGGGGATGGACAGCGCGCTGTGGCC	4320
Qy	4321	TTTAAGGTCATGAGCGGCGAGATGCCCTCCACCGAGACTGTGGCTAACCTACTCTCTCT	4380
Db	4321	TTTAAGGTCATGAGCGGCGAGATGCCCTCCACCGAGACTGTGGCTAACCTACTCTCTCT	4380
Qy	4381	ATCCCTCTCCCTGGCGGCTAGTCGTCTGGGGGTGTGTGGCGACGCAATGATGGCTGGCAC	4440
Db	4381	ATCCCTCTCCCTGGCGGCTAGTCGTCTGGGGGTGTGTGGCGACGCAATGATGGCTGGCAC	4440
Qy	4441	GTGGGCCCCAGGGGAGGGGGCTGTGCAGTGGATGACCGGCTGTATAGCCTTGCTTCGCGG	4500
Db	4441	GTGGGCCCCAGGGGAGGGGGCTGTGCAGTGGATGACCGGCTGTATAGCCTTGCTTCGCGG	4500
Qy	4501	GGTAAACCAACGCTCCCGCCAGCACAATGTATCCGTAAGGAGCAGCTGCACAGCTTCACT	4560
Db	4501	GGTAAACCAACGCTCCCGCCAGCACAATGTATCCGTAAGGAGCAGCTGCACAGCTTCACT	4560
Qy	4561	CAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTACCAGATGGATCAAC	4620
Db	4561	CAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTACCAGATGGATCAAC	4620
Qy	4621	GAGGACTCCTCCACGCGCATCTCCGCGCTGGCTTAAGAGATGTTGGATTGATATAGC	4680
Db	4621	GAGGACTCCTCCACGCGCATCTCCGCGCTGGCTTAAGAGATGTTGGATTGATATAGC	4680
Qy	4681	ACGGTGTGACTGATTTTCAAGACCTGGCTCAAGTCCAACTCCTGCGCGATTGGCGGGA	4740
Db	4681	ACGGTGTGACTGATTTTCAAGACCTGGCTCAAGTCCAACTCCTGCGCGATTGGCGGGA	4740
Qy	4741	GTCCCTCTCTCATATGTCAACGATGGGTAAAGGAGTGTGGCGGGGACACGCGATCATG	4800
Db	4741	GTCCCTCTCTCATATGTCAACGATGGGTAAAGGAGTGTGGCGGGGACACGCGATCATG	4800
Qy	4801	CAAAACACCTGCCCATGTGGAGCACAGATACCGGACATGTGAAAAAAGTTCATAGAG	4860
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    |||

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RESULT 12

AAD25324 standard; cDNA; 7987 BP.

AAD25324;

12-MAR-2002 (first entry)

Hepatitis C virus (HCV) adaptive replicon VI cDNA mutant.

Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
 adaptive replicon VI; mutant; ss.

Hepatitis C virus.

Hepatitis C virus.

Hepatitis C virus.

Hepatitis C virus.

Location/Qualifiers
 1801..7758
 /tag- a
 /product- "HCV adaptive replicon VI protein"
 4642..5982
 /tag- b
 /product- "NS5A protein of HCV adaptive replicon VII"

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FT /note= "CDS does not include both start and stop
FT codon"
FT /partial
FT mutation (5336, G)
    /tag- c
PN WC200189364-A2.
XX 29-NOV-2001.
PD 23-MAY-2001: 2001MO-US16822.
PE 23-MAY-2000: 2000US-0576989.
XX 23-MAY-2000: 2000US-0576989.
XX (UNIW ) UNIV WASHINGTON.
PA Rice CM, Blight RJ;
PI WPI: 2002-066755/09.
XX P-FSDB: AAE15720, AAE15721.
DR
XX Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage; useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences
PS Disclosure; Page 74-77; 174pp; English.
XX
XX The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets.
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficiency replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays.
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated or defective HCV derivatives as possible vaccine candidates, engineering of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) adaptive replicon VI cDNA mutant. This sequence
CC is generated by the mutation 9 to t at position 5336 of
CC HCVrepIDBarlman/Availi cDNA.
XX
SO Sequence 7987 BP; 1646 A; 2368 C; 2243 G; 1730 T; 0 other;
Query Match 99.7%; Score 7965.4; DB 24; Length 7987;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7981; Conservative 0; Mismatches 6; Indels 2; Gaps 1.
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QY 5341 CTGTGTGCGCTTCTTAAAGCAACATGCACTACCTGCTATGCTCCCGGAGCGTGC 5400
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Db 5341 CTGTGTGCGCTTCTTAAAGCAACATGCACTACCTGCTATGCTCCCGGAGCGTGC 5400
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Db 5401 CTGATCGAGGCAACCTCTGTGGGGAGAGATGGGCGGAGCATCACCGCGTGGAG 5460
QY 5461 TCAGAAATTAAGTAAATTTTGGACTTTTCAAGCCGCTCCAGGCGAGAGAGATGAG 5520
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QY 5521 AAGGAATATCCGTCGCGGGAGATCTCGGAGGTCAGAGAAATTCCTCGAGCGATG 5580
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Db 5521 AAGGAATATCCGTCGCGGGAGATCTCGGAGGTCAGAGAAATTCCTCGAGCGATG 5580
QY 5581 CCCATATGGGCAAGCCGAGATTACAACTCCACTGTTAGAGTCTTGAAGAGACCCGGAC 5640
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Db 5581 CCCATATGGGCAAGCCGAGATTACAACTCCACTGTTAGAGTCTTGAAGAGACCCGGAC 5640
QY 5641 TACGTCCTCCAGTGGTACAGGGGTGCTATGCGGCTGCGCAAGGCGCTCCGATATCA 5700
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Db 5641 TACGTCCTCCAGTGGTACAGGGGTGCTATGCGGCTGCGCAAGGCGCTCCGATATCA 5700
QY 5701 CCTCCAGAGAGAGAGAGGTTGCTCTGCAAAATCTACCGTGTCTTCTGCTTGGCG 5760
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QY 5701 CCTCCAGAGAGAGAGAGGTTGCTCTGCAAAATCTACCGTGTCTTCTGCTTGGCG 5760
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QY 5761 GAGCTCCGCAAGAGACTTGGAGCTCGGAATCGTCGGCGGTGAGACAGGCGAGGCA 5820
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QY 6061 ACAGGCGCTGATCAGCCATGCGCTGCGGAGAGAAACAACTGCCCATTAATGACTG 6060
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QY 6481 GTTCAAGCAAGAAAGGCGCGGCAAGCAAGCTGCTTACGATTTCCAGATTGGGG 6480
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Db 6721 CCCGAAGCCAGACAGGCCATTAAAGTGGCTCACAGAGCGGCTTTACATGTGGGGGCCCTG 6780
Qy 6781 ACTAATTTAAAGGAGACAGTCCGCTATGCCGGTCCGGGAGAGGGGTACTGACG 6840
Db 6781 ACTAATTTAAAGGAGACAGTCCGCTATGCCGGTCCGGGAGAGGGGTACTGACG 6840
Qy 6841 ACCAGTGGCGATATACCTTCACATGTTACTTGAAGCCGCTGCGGCTGTGACGTGCG 6900
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Db 7201 TCCGAGCTAGAGCAATCATCATGTATGCGCCACCTTGTGGGCAAGAGATGCTGATG 7260
Qy 7261 ACTCATTTCTTCCATCTCTTCTAGCTCAGGAACAATTGAAAGAGAGAGAGAGAGAGAGAG 7320
Db 7261 ACTCATTTCTTCCATCTCTTCTAGCTCAGGAACAATTGAAAGAGAGAGAGAGAGAGAG 7320
Qy 7321 ATCTAGGGGGGCTTACTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7380
Db 7321 ATCTAGGGGGGCTTACTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7380
Qy 7381 CATGCGCTTAGCGCATTTTCTACTCATAGTACTCTCCAGAGTGAATAGAGTGGCT 7440
Db 7381 CATGCGCTTAGCGCATTTTCTACTCATAGTACTCTCCAGAGTGAATAGAGTGGCT 7440
Qy 7441 TCAAGCCTCAGAAACTGAGGAGTACCGGCTTGGAGTGGAGATGAGAGAGAGAGAGAGAGAG 7500
Db 7441 TCAAGCCTCAGAAACTGAGGAGTACCGGCTTGGAGTGGAGATGAGAGAGAGAGAGAGAGAG 7500
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Db 7501 GTCCGCGCTAGGCTACTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7560
Qy 7561 AACTGGGAGTAAAGAGCAAGCTCAAACTCACTCAATCCCGGCTGCGTCCAGTTGGAT 7620
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Db 7621 TTATCAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 7680
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Qy 7741 CTATCCCGCAACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7800
Db 7741 CTATCCCGCAACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7800
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Qy 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Qy 7861 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7859 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7918
Qy 7921 TACTGTGAAGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7980
Db 7919 TACTGTGAAGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7978
Qy 7981 AGATCAAGT 7989
Db 7979 AGATCAAGT 7987

RESULT 13
ID AAL47278 standard; DNA; 7995 BP.
XX AAL47278;
AC AAL47278;
XX 30-AUG-2002 (first entry)
DE Hepatitis C virus sub-genomic replicon recombinant clone HCV8.
XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
KM virulence; hepatotropic; gene therapy; anti-viral; gene; ds.
XX Hepatitis C virus.
OS Hepatitis C virus.
XX WO200238793-A2.
XX 16-MAY-2002.
XX 02-NOV-2001; 2001MO-US46350.
XX PF 07-NOV-2000; 2000US-245866P.
XX PR (ANAD-) ANADYS PHARM INC.
XX PA Bichko V.
XX PI WPI: 2002-490082/52.
XX DR Novel nucleic acid encoding replication competent recombinant hepatitis
XX PT C virus genome useful for screening anti-hepatitis C virus therapeutics
XX PT and for vaccine development
XX PS Claim 8; Page 56-61; 85pp; English.
XX XX The present invention provides protein and coding sequences from
XX CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
XX CC able to replicate efficiently when transfected into a susceptible cell
XX CC line without reducing the growth rate of the cell line by more than 10
XX CC fold. The sequences are useful for screening for anti-HCV therapeutics,
XX CC for detecting antibodies to HCV in a biological sample such as blood,
XX CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
XX CC for deriving authentic HCV components such as replication-competent
XX CC non-infectious, replication-defective infection component, and
XX CC replication-defective non-infectious HCV. In gene therapy, or gene
XX CC vaccination targeted to hepatic tissue for treating an animal infected or
XX CC susceptible to HCV infection and for studying HCV infection and
XX CC propagation. The present sequence is a clone of a fragment of the HCV
XX CC genome designated HCV8.
XX XX Sequence 7995 BP; 1650 A; 2367 C; 2243 G; 1735 T; 0 other:
SQ

Query Match 99.6%; Score 7961.4; DB 24; Length 7995;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7981; Conservative 0; Mismatches 11; Indels 3; Gaps 1;
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QY 1 GCCAGCCCCGATTTGGGGGCGACACTCCACCATAGTACCTCCCTGTGAGAACTACTG 60
Db 1 GCCAGCCCCGATTTGGGGGCGACACTCCACCATAGTACCTCCCTGTGAGAACTACTG 60
QY 61 TCTTCAGAGAAAGGCTTACCCATGGGCTAGTATGATGCTGTGACCTCCAGAC 120
Db 61 TCTTCAGAGAAAGGCTTACCCATGGGCTAGTATGATGCTGTGACCTCCAGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACCGGAATTGCGAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACCGGAATTGCGAG 180
QY 181 GAGAGCCGGGTCTTCTTCTTGATCAACCCGCTCAATGCCGTGAGATTTGGGCGTGC 240
Db 181 GAGAGCCGGGTCTTCTTCTTGATCAACCCGCTCAATGCCGTGAGATTTGGGCGTGC 240
QY 241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAGGCTTGTGACTGCTGATAGG 300
Db 241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAGGCTTGTGACTGCTGATAGG 300
QY 301 GTGCTTGCAGATGCCCGGAGAGTCTGATAGCCGTGCACATGAGCAGATCCTAAAC 360
Db 301 GTGCTTGCAGATGCCCGGAGAGTCTGATAGCCGTGCACATGAGCAGATCCTAAAC 360
QY 361 CTCGAAGAAACCAAGAGGCGCGCATGATTGAACAGATGGATTGGACGCAAGTTCTC 420
Db 361 CTCGAAGAAACCAAGAGGCGCGCATGATTGAACAGATGGATTGGACGCAAGTTCTC 420
QY 421 CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
Db 421 CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
QY 481 CTGATGCCGCGTGTCCGGCTGTGAGGGCAGGGGCGCGGCTCTTTTCTCAAGACC 540
Db 481 CTGATGCCGCGTGTCCGGCTGTGAGGGCAGGGGCGCGGCTCTTTTCTCAAGACC 540
QY 541 ACCGTGCGGTGCTTGAATGAACTGACAGAGAGGAGCGCGCTATCGTGCTGAGCA 600
Db 541 ACCGTGCGGTGCTTGAATGAACTGACAGAGAGGAGCGCGCTATCGTGCTGAGCA 600
QY 601 CGAGGGGCTTCTTGGGAGCTGTGCGAGCTGTGCGAGCTGTGACGAGCGGGAAGGACTGCG 660
Db 601 CGAGGGGCTTCTTGGGAGCTGTGCGAGCTGTGCGAGCTGTGACGAGCGGGAAGGACTGCG 660
QY 661 TGCATTTGGGCGAAGTGCOCGGGCGAGATCTCTGTCACTTCACTTGTCTGCGAGA 720
Db 661 TGCATTTGGGCGAAGTGCOCGGGCGAGATCTCTGTCACTTCACTTGTCTGCGAGA 720
QY 721 AAGTATCCATGATGGCTGATGCAATGCGGGCGCTGCAATACGCTTGATCCGCTACCTGCG 780
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QY 781 CATTCGACCAACCAAGCAATGCGATGAGCAGAGACGTAAGTCCGATGGAAGCCGCTG 840
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QY 841 TTGTGATCAGATGATGTCGAGCAAGAGCATGAGGGCTGCGCCACGCCAAGTCTTG 900
Db 841 TTGTGATCAGATGATGTCGAGCAAGAGCATGAGGGCTGCGCCACGCCAAGTCTTG 900
QY 901 CCAGGCTCAAGGCGGAGTGCOCGCGAGGCGAGATCTGAGTACCATGGGAGTACCT 960
Db 901 CCAGGCTCAAGGCGGAGTGCOCGCGAGGCGAGATCTGAGTACCATGGGAGTACCT 960
QY 961 GCTTGGCGAATATCATGTTGAAAAATGCGCTTTCTGATTCATGACTGTGGCGCG 1020
Db 961 GCTTGGCGAATATCATGTTGAAAAATGCGCTTTCTGATTCATGACTGTGGCGCG 1020
QY 1021 TGGGTGTGGCGGAGCGCTATCAGGACATAGGCTGAGTACCGCGTATGATTTGAAAGAGC 1080
Db 1021 TGGGTGTGGCGGAGCGCTATCAGGACATAGGCTGAGTACCGCGTATGATTTGAAAGAGC 1080
QY 1081 TTGGGGCGAATGGGCTGACCGGCTTCTGCTGCTTTACGGTATCGCGCTCCGATTCGC 1140
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Db 1141 AGCGATGCGCTTCTATGCGCTTCTTGACGAGTTCTTGAGTGTAAACAGACCAACAG 1200
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Db 1321 CCGTCTTTGGCAATGTAGGGGCGCGGAACCTGAGCCCTGCTCTTGACGAGATTCCT 1380
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Db 1621 TGGCTCTCCTCAAGCGTATTCAACAAGGGGTGGAAGGTGCGCGAAGGATACCCATTGT 1680
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Db 1681 ATGGGATGATCTGTGGGCTCTGCGTGCATGCTTTACATGTGTTTGTGAGGATTA 1740
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Db 1741 AACGCTAGAGCCCCCGCAACAGAGGAGCGGTTTTCCTTTGAAGAAACGATTAATAC 1800
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Db 1801 ATGGGCGCTATTACGGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCT 1860
QY 1861 ACCCTCACAGGCGGGAAGCAACAGAGTGAAGGGAGAGTCCAGGTGCTCACCGCA 1920
Db 1861 ACCCTCACAGGCGGGAAGCAACAGAGTGAAGGGAGAGTCCAGGTGCTCACCGCA 1920
QY 1921 ACACAATCTTTCCTGCGACCTGCTCAATGAGCTGTGTTGAGCTGTCTATCATGAGGCC 1980
Db 1921 ACACAATCTTTCCTGCGACCTGCTCAATGAGCTGTGTTGAGCTGTCTATCATGAGGCC 1980
QY 1981 GSGCTCAAGACCTTGGCGGCGCCAAAGGGCCCAATTCACCAATGTACACCAATGTGAC 2040
Db 1981 GSGCTCAAGACCTTGGCGGCGCCAAAGGGCCCAATTCACCAATGTACACCAATGTGAC 2040
QY 2041 CAGGACCTGCTGCGCTGCAAGCGCCCCCGGGCGGCTTCTTGAACACATGCACCTG 2100
Db 2041 CAGGACCTGCTGCGCTGCAAGCGCCCCCGGGCGGCTTCTTGAACACATGCACCTG 2100
QY 2101 GGCAGCTGGAACCTTTACTTGTGTACGAGGACATGCCATGTCAATTCGCGGCGCGCG 2160
Db 2101 GGCAGCTGGAACCTTTACTTGTGTACGAGGACATGCCATGTCAATTCGCGGCGCGCG 2160
QY 2161 GCGCAGCAGAGGGGAGCTACTCTCCCGAGCGCTGCTCACTTGAAGGCGCTTTCG 2220

D	2161	GGGAGACAGCAGGGGGAGCCTACTCTCCCAAGGCCCGCTCTCACTGAAAGGCGCTCTTCG	2220
O	2221	GGCGGTCACACTGCTCTGCCCTTCGGGGAGACGCTGTGGGCATCTTTTCGGGCTGCCGTGTGC	2280
D	2221	GGGGGTCCACTGCTCTGCCCTTCGGGGAGACGCTGTGGGCATCTTTTCGGGCTGCCGTGTGC	2280
O	2281	ACCCGAGGGTTTCCGAGAGGCGGTGGACCTTTGTACCCCGTCAGTCTATAGGAAACCACTATAG	2340
D	2281	ACCCGAGGGTTTCCGAGAGGCGGTGGACCTTTGTACCCCGTCAGTCTATAGGAAACCACTATAG	2340
O	2341	CGGTCCCGGCTCTTCACGAGCAACTGTCCTCCGGCCGTACCGCAGACATTCACAGTTC	2400
D	2341	CGGTCCCGGCTCTTCACGAGCAACTGTCCTCCGGCCGTACCGCAGACATTCACAGTTC	2400
O	2401	GCCCATCTACAGCCCCCTCTCTGCTAGCGGCAAGACACTATAGGTGGCGGCTGGGTATAGCA	2460
D	2401	GCCCATCTACAGCCCCCTCTCTGCTAGCGGCAAGACACTATAGGTGGCGGCTGGGTATAGCA	2460
O	2461	GCCCAAGGATATAGGTGCTGTCTGCTGAAACCCGCTCCGTCCGCGCACCTTAGTTCGGG	2520
D	2461	GCCCAAGGATATAGGTGCTGTCTGCTGAAACCCGCTCCGTCCGCGCACCTTAGTTCGGG	2520
O	2521	GGCTATATGCTTAAAGGACATGGTATCGACCTTAACATCAAGACCGGGGTAAAGACCATTC	2580
D	2521	GGCTATATGCTTAAAGGACATGGTATCGACCTTAACATCAAGACCGGGGTAAAGACCATTC	2580
O	2581	ACCAAGGATGCCCACTACACAGTACTCCACTATGGCAAGTTCTCTGCGACGGTGTGTGC	2640
D	2581	ACCAAGGATGCCCACTACACAGTACTCCACTATGGCAAGTTCTCTGCGACGGTGTGTGC	2640
O	2641	TCTGGGGGGCGCTATGACATCAATAATGTGATGTGTCGACTCAACTAAGTATGATGACACT	2700
D	2641	TCTGGGGGGCGCTATGACATCAATAATGTGATGTGTCGACTCAACTAAGTATGATGACACT	2700
O	2701	ATCTCGGGCATCGGCACAGTCCCTGAGCAAGGGGAGAGCGCTGAGCGCGACTGTCGTG	2760
D	2701	ATCTCGGGCATCGGCACAGTCCCTGAGCAAGGGGAGAGCGCTGAGCGCGACTGTCGTG	2760
O	2761	CTCGGCACCGCTACGCTCCGGGATCGGTCACCGTACCGATCCCAATCGAAGAGAGGTG	2820
D	2761	CTCGGCACCGCTACGCTCCGGGATCGGTCACCGTACCGATCCCAATCGAAGAGAGGTG	2820
O	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGGCCATCCCATCGAGACATTC	2880
D	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGGCCATCCCATCGAGACATTC	2880
O	2881	AAGGGGGGAGAGCAACCTATTTCTGCAATCCAAACAAATGTGATGACTGCGCGG	2940
D	2881	AAGGGGGGAGAGCAACCTATTTCTGCAATCCAAACAAATGTGATGACTGCGCGG	2940
O	2941	AAGCTGTCCGGCTTCGAGTCAATGCTGTAGCATATTAACGGGGCTTGAATGATCCGTC	3000
D	2941	AAGCTGTCCGGCTTCGAGTCAATGCTGTAGCATATTAACGGGGCTTGAATGATCCGTC	3000
O	3001	ATACCAACTACGAGACGTCATTTGCTGTAGCAACGAGCGCTCTAATACGGGCTTTCAC	3060
D	3001	ATACCAACTACGAGAGACGTCATTTGCTGTAGCAACGAGCGCTCTAATGAGCGGCTTTCAC	3060
O	3061	GCGCATTTTCGACTAGTATGACATGCAATACATGTGTACCCAGACAGTGCATCTACG	3120
D	3061	GCGCATTTTCGACTAGTATGACATGCAATACATGTGTACCCAGACAGTGCATCTACG	3120
O	3121	CTGGACCGGACTTCACATTTGAGACAGACACCGTCCCAAGACAGCGGCTGCAGCTGC	3180
D	3121	CTGGACCGGACTTCACATTTGAGACAGACACCGTCCCAAGACAGCGGCTGCAGCTGC	3180
O	3181	CAGCGCGCAGCAGCACTGTGTAGGGGAGAGATGGGCAATTAAGGTTTGTGACTCCAGGA	3240
D	3181	CAGCGCGCAGCAGCACTGTGTAGGGGAGAGATGGGCAATTAAGGTTTGTGACTCCAGGA	3240
O	3241	GAAGCGCCCTGGGATTTGATCTCTCGTTCTGTGAGAGGATATGACCGCGGCTGT	3300
D	3241	GAAGCGCCCTGGGATTTGATCTCTCGTTCTGTGAGAGGATATGACCGCGGCTGT	3300

Db	3241	GAAGGGCCCTCG866CATGTTCCATTCCTCCGGTTCTGTCCAGATGCTATGACGGGGGCTG	3300
Qy	3301	GCTTGTAGACAGCTCAAGCCCGCCGAGACCTCAGTTAGTTGGGGCTTACCTTAACACA	3360
Db	3301	GCTTGTAGACAGCTCAAGCCCGCCGAGACCTCAGTTAGTTGGGGCTTACCTTAACACA	3360
Qy	3361	CGAAGGTGGCCCTCGCCAGGACCATCGAGTCTGSGGAGCGTCTTTACAGGCTC	3420
Db	3361	CGAAGGTGGCCCTCGCCAGGACCATCGAGTCTGSGGAGCGTCTTTACAGGCTC	3420
Qy	3421	ACCCACATAGACGCCATTTTCTTGTGCCAGACTAAGACAGGAGAGCAACTTCCCTAC	3480
Db	3421	ACCCACATAGAGGCCCATTTTCTTGTGCCAGACTAAGACAGGAGAGCAACTTCCCTAC	3480
Qy	3481	CTGTGTACATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGAC	3540
Db	3481	CTGTGTACATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGAC	3540
Qy	3541	CAATGTGGAAGTGTCTCATACGGGCTAAAGCCCTACGTGCAGCGGGCCAAACGCCCTCTG	3600
Db	3541	CAATGTGGAAGTGTCTCATACGGGCTAAAGCCCTACGTGCAGCGGGCCAAAGCCCTCTG	3600
Qy	3601	TATAGGCTGGAGGCCCTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATACATC	3660
Db	3601	TATAGGCTGGAGGCCCTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATACATC	3660
Qy	3661	ATGGCATGCAATGTCGGCTGACCCGAGAGTCTGACAGAGACCTGGGTCGTGTAGCGGA	3720
Db	3661	ATGGCATGCAATGTCGGCTGACCCGAGAGTCTGACAGAGACCTGGGTCGTGTAGCGGA	3720
Qy	3721	GTCCTAGACAGCTCTGGCCCGATTTCTCCTGACACAGGACGAGCGTGCTATTGTGAGCAG	3780
Db	3721	GTCCTAGACAGCTCTGGCCCGATTTCTCCTGACACAGGACGAGCGTGCTATTGTGAGCAG	3780
Qy	3781	ATCATCTTGTCCGGAAGGCCGGCCATCTCCCGACAGGGAAGTCTTTACCGGAGTTC	3840
Db	3781	ATCATCTTGTCCGGAAGGCCGGCCATCTCCCGACAGGGAAGTCTTTACCGGAGTTC	3840
Qy	3841	GATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATGGAACAGGGAATCAGACTGCC	3900
Db	3841	GATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATGGAACAGGGAATCAGACTGCC	3900
Qy	3901	GACACATTCAAACGAAGGCAATCGGGTGTCTGCAAAACGCCACCAACAAGCCGAGGCT	3960
Db	3901	GACACATTCAAACGAAGGCAATCGGGTGTCTGCAAAACGCCACCAACAAGCCGAGGCT	3960
Qy	3961	GCTGCTCCCGTGTGGAATCCAAGTGGCGGACCTCGAAGCCTTGTGGGCGAAGCATATG	4020
Db	3961	GCTGCTCCCGTGTGGAATCCAAGTGGCGGACCTCGAAGCCTTGTGGGCGAAGCATATG	4020
Qy	4021	TGGAAATTCATACGGGGATPACAAATATTTAGAGGCTTGTCCACTCTGCTTGGCAACCC	4080
Db	4021	TGGAAATTCATACGGGGATPACAAATATTTAGAGGCTTGTCCACTCTGCTTGGCAACCC	4080
Qy	4081	GGGATAGCATACAGTGAATGGCAATTCAGGCTCTATACACAGCCCGCTACACACCAAT	4140
Db	4081	GGGATAGCATACAGTGAATGGCAATTCAGGCTCTATACACAGCCCGCTACACACCAAT	4140
Qy	4141	ACCCTCCTGTTTAAACATCTGTGGGGATGGGAGGCCCCCAACTGTCTCTCCAGGCT	4200
Db	4141	ACCCTCCTGTTTAAACATCTGTGGGGATGGGAGGCCCCCAACTGTCTCTCCAGGCT	4200
Qy	4201	GCTTCTGCTTTCGTAAGCGCCCGGATGCGTGGAGCGGCTGTGTGGACATAGAGCTTGG	4260
Db	4201	GCTTCTGCTTTCGTAAGCGCCCGGATGCGTGGAGCGGCTGTGTGGACATAGAGCTTGG	4260
Qy	4261	AAGGTCTTGAGATATTTTGGAGGTTATAGAGCAAGGGGTGGCAGGCGCGCTGTGGCC	4320
Db	4261	AAGGTCTTGAGATATTTTGGAGGTTATAGAGCAAGGGGTGGCAGGCGCGCTGTGGCC	4320
Qy	4321	TTTAAAGTCATAGCGCGAGATGCCCTCCACCGAGAGCTGGCTAACTACTCCCTCT	4380
Db	4321	TTTAAAGTCATAGCGCGAGATGCCCTCCACCGAGAGCTGGCTAACTACTCCCTCT	4380

QY	4381	ATCTCTCCCTTGAGCGCCCTTAAGTGTCTGGGGGTCTGTGTGTGGACAGCAATACTGGCTGGCAC	4440
Db	4381	ATCTCTCCCTTGAGCGCCCTTAAGTGTCTGGGGGTCTGTGTGTGGACAGCAATACTGGCTGGCAC	4440
QY	4441	GTGGGCCACGAGGGAGGGGCGCTGTGCAGTGGATGAACCGGCTATAGCTTGCTTCGCGG	4500
Db	4441	GTGGGCCACGAGGGAGGGGCGCTGTGCAGTGGATGAACCGGCTATAGCTTGCTTCGCGG	4500
QY	4501	GGTAACCAAGTCTCCCCACAGCACTATGTGCTGTGAGAGGAGCGCTGACACAGTGTACT	4560
Db	4501	GGTAACCAAGTCTCCCCACAGCACTATGTGCTGTGAGAGGAGCGCTGACACAGTGTACT	4560
QY	4561	CAGATCTCTTATGTCTTATACATCACTAGCTGCTGAAGAGGCTTCACCAAGTATCAAC	4620
Db	4561	CAGATCTCTTATGTCTTATACATCACTAGCTGCTGAAGAGGCTTCACCAAGTATCAAC	4620
QY	4621	GAGAGCTGCTCCACAGCCATCTTCGCGCTGTGGGCTAAGAGATGTGGATTTGGATATAGC	4680
Db	4621	GAGAGCTGCTCCACAGCCATCTTCGCGCTGTGGGCTAAGAGATGTGGATTTGGATATAGC	4680
QY	4681	ACGGTGTGACTGATTTCAAGAGCTGGCTCCAGTCCAGCTCTCCCGATTTGCCGGGA	4740
Db	4681	ACGGTGTGACTGATTTCAAGAGCTGGCTCCAGTCCAGCTCTCCCGATTTGCCGGGA	4740
QY	4741	GTCCCTCTTCTCATATGTCAACGTGGTACMAAGGATGTGGCGGGGCGACGGCTATG	4800
Db	4741	GTCCCTCTTCTCATATGTCAACGTGGTACMAAGGATGTGGCGGGGCGACGGCTATG	4800
QY	4801	CAAAACACCTGCCCATGTGGAGCAGATTCACCGACATGTGAAAAA--GGTTCATG	4857
Db	4801	CAAAACACCTGCCCATGTGGAGCAGATTCACCGACATGTGAAAAA--GGTTCATG	4857
QY	4858	AGATCTGTGGGGCTTAGGACTCTAGTAACAGTGGCATGAGAACTCCCATTTAGCG	4917
Db	4858	AGATCTGTGGGGCTTAGGACTCTAGTAACAGTGGCATGAGAACTCCCATTTAGCG	4917
QY	4918	TACACACGAGGCCCTTGACAGCGCTCCCGGCGCCAAATATTCTAGGGCGCTGTGGCG	4977
Db	4918	TACACACGAGGCCCTTGACAGCGCTCCCGGCGCCAAATATTCTAGGGCGCTGTGGCG	4977
QY	4978	GTGCTCTGTAGAGTACGTGAGAGGTTACGGGGGTGGGGATTCTCCACTAGCTGACGGGC	5037
Db	4978	GTGCTCTGTAGAGTACGTGAGAGGTTACGGGGGTGGGGATTCTCCACTAGCTGACGGGC	5037
QY	5038	ATGACCACTGACAAAGTAAAGTCCCGTGTGAGGTTCCGGCCCGGAAATTTTTCACAGA	5097
Db	5038	ATGACCACTGACAAAGTAAAGTCCCGTGTGAGGTTCCGGCCCGGAAATTTTTCACAGA	5097
QY	5098	GTGATGAGGGGCGGTTGACAGGTACGTGCGAGCTGTGAACCCCTCTTAGGGAGAGG	5157
Db	5098	GTGATGAGGGGCGGTTGACAGGTACGTGCGAGCTGTGAACCCCTCTTAGGGAGAGG	5157
QY	5101	GTGATGAGGGGCGGTTGACAGGTACGTGCGAGCTGTGAACCCCTCTTAGGGAGAGG	5160
Db	5101	GTGATGAGGGGCGGTTGACAGGTACGTGCGAGCTGTGAACCCCTCTTAGGGAGAGG	5160
QY	5158	GTCACTATCTGTGTGGGCTCAATCAATACGTGTTGGTGTACAGTCCCATGTGAGGCC	5217
Db	5158	GTCACTATCTGTGTGGGCTCAATCAATACGTGTTGGTGTACAGTCCCATGTGAGGCC	5217
QY	5218	GAAACGAGAGTGTGACGTCTTCATTCATGCTACAGGAGCCCTCCACATTACGGCGAG	5277
Db	5218	GAAACGAGAGTGTGACGTCTTCATTCATGCTACAGGAGCCCTCCACATTACGGCGAG	5277
QY	5278	ACGGCTAAGCGTAAAGTGTGGCCAGGGAGTCTCCCGCTCTTGAGCAAGCTCATCACTAGC	5337
Db	5278	ACGGCTAAGCGTAAAGTGTGGCCAGGGAGTCTCCCGCTCTTGAGCAAGCTCATCACTAGC	5337
QY	5338	CAGTGTCTGGGCTTCTCTTGAAGGAACGTGACATACCGTATGACTTCCCGGAGCT	5397
Db	5338	CAGTGTCTGGGCTTCTCTTGAAGGAACGTGACATACCGTATGACTTCCCGGAGCT	5397
QY	5341	CAGTGTCTGGGCTTCTCTTGAAGGAACGTGACATACCGTATGACTTCCCGGAGCT	5400
Db	5341	CAGTGTCTGGGCTTCTCTTGAAGGAACGTGACATACCGTATGACTTCCCGGAGCT	5400
QY	5386	GACCTCATCGAGGCAACCTCTGTGTGGCGGAGAGATGGCGGGAATCAACCCGCGTG	5457
Db	5401	GACCTCATCGAGGCAACCTCTGTGTGGCGGAGAGATGGCGGGAATCAACCCGCGTG	5460

QY	5458	GAGTCAGCAAAATAAGTAGTAACTAATTTTGGACTCTTTTGAGCCGCTCCAAAGCGAGAGCAT	5517
Db	5461	GAGTCAGCAAAATAAGTAGTAAATTTTGGACTCTTTTGAGCCGCTCCAAAGCGAGAGCAT	5520
QY	5518	GAGAGGAGAAATATCCGTTCCGCGGAGATCTGCGAGGATCCAGGAAATTCCTCTGAGCG	5577
Db	5521	GAGAGGAGAAATATCCGTTCCGCGGAGATCTGCGAGGATCCAGGAAATTCCTCTGAGCG	5580
QY	5578	ATGGCCATATGGGACGCCCGGATTTACAAACCTCCACTGTAGAGTCTTGGAAAGAACCCG	5637
Db	5581	ATGGCCATATGGGACGCCCGGATTTACAAACCTCCACTGTAGAGTCTTGGAAAGAACCCG	5640
QY	5638	GACTACGTCCCTCCAGTAGTGATACAGGGGTGTCCATTGCCCGCTCCAAAGGCCCTCCGATA	5697
Db	5641	GACTACGTCCCTCCAGTAGTGATACAGGGGTGTCCATTGCCCGCTCCAAAGGCCCTCCGATA	5700
QY	5698	CCACTCTCCAGGAGGAGAGAGGAGGTTGTCCTGAGATCTAACGTGCTTCCTGACTG	5755
Db	5701	CCACTCTCCAGGAGGAGAGGAGGTTGTCCTGAGATCTAACGTGCTTCCTGACTG	5766
QY	5758	GCGAGAGCTCGCCACAAGACCTTCGCGAGCTCGAATCTGCGAGCGTGCAGCGGGACG	5817
Db	5761	GCGAGAGCTCGCCACAAGACCTTCGCGAGCTCGAATCTGCGAGCGTGCAGCGGGACG	5820
QY	5818	GCAAGCGCTCTCTCTGACACAGCCCTCCGAGACGGGAGAGGGGATCCGAGCTTAGTGC	5877
Db	5821	GCAAGCGCTCTCTCTGACACAGCCCTCCGAGACGGGAGAGGGGATCCGAGCTTAGTGC	5880
QY	5878	TACTCTCCATGCCCCCTTTGAGGGGGAGCCGGGGGATCCCGATCTACGACAGGGTCT	5937
Db	5881	TACTCTCCATGCCCCCTTTGAGGGGGAGCCGGGGGATCCCGATCTACGACAGGGTCT	5940
QY	5938	TGGTCTACCCGTAACCGAGGAGGGGTAGTGAAGACGTCTGTGGTGCCTGATGTCTACACA	5997
Db	5941	TGGTCTACCCGTAACCGAGGAGGGGTAGTGAAGACGTCTGTGGTGCCTGATGTCTACACA	6000
QY	5998	TGACAGAGCGCCCTGATCACGCCATGCGGTGCGGAGGAAACCAAGCTGCCATCAATGCA	6057
Db	6001	TGACAGAGCGCCCTGATCACGCCATGCGGTGCGGAGGAAACCAAGCTGCCATCAATGCA	6060
QY	6058	CTGAGCAACTTTTGTCTCCGTCACACACAATTGTTGTATGTACCAACTCTGCGACGGA	6117
Db	6061	CTGAGCAACTTTTGTCTCCGTCACACACAATTGTTGTATGTACCAACTCTGCGACGGA	6120
QY	6118	AGCCTGCGGCGAGAANGTTCACCTTTGACAGACTCGAGGTCTGTGAGCACACTAACGG	6177
Db	6121	AGCCTGCGGCGAGAANGTTCACCTTTGACAGACTCGAGGTCTGTGAGCACACTAACGG	6180
QY	6178	GACGCTCAAGAGATGAGAGGGGAGGCGTCACAGTTAAAGCTTAACTTTATTCGCG	6233
Db	6181	GACGCTCAAGAGATGAGAGGGGAGGCGTCACAGTTAAAGCTTAACTTTATTCGCG	6246
QY	6238	GAGGAAGCTGTAAAGTACGAGCCGCCACATTCGCGCAGATCTAAATTTGCTATGGGCA	6297
Db	6241	GAGGAAGCTGTAAAGTACGAGCCGCCACATTCGCGCAGATCTAAATTTGCTATGGGCA	6300
QY	6298	AAGAGCGTCGAGACATCTATCCAGACAGGCGGTATACCAATCCGCTCGCTGTGAAGGAC	6357
Db	6301	AAGAGCGTCGAGACATCTATCCAGACAGGCGGTATACCAATCCGCTCGCTGTGAAGGAC	6366
QY	6358	TTGCTGGAAGACTGTGAGACACAATTGACACCACCATATGGCAAAAATAGATTTTC	6417
Db	6361	TTGCTGGAAGACTGTGAGACACAATTGACACCACCATATGGCAAAAATAGATTTTC	6420
QY	6418	TGCCTCAACACAGAGAGGGGGGCGCAACCAACGCTGCGCTATCTATTCACAATTG	6477
Db	6421	TGCCTCAACACAGAGAGGGGGGCGCAACCAACGCTGCGCTATCTATTCACAATTG	6480
QY	6478	GGGTTGTGTGTCTCGAGAAAATAGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGC	6537
Db	6481	GGGTTGTGTGTCTCGAGAAAATAGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGC	6540
QY	6538	GTGATGGGCTTTCATATAGGATTCACAATATCTCTCGAGAGGCGGGTCAAGTTCTCGTG	6597


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Db 5541 GTATGATGGGCTCTCATAGAGATTCACATCTCTCCGAGACAGCGGGTGCAGATTCCTGGTG 6600
QY 6598 AATGCTGGAAAGCGAAGAAATGCGCTATGGCTTCGCATATGACACCCGCTGTTTAC 6657
Db 6601 AATGCTGGAAAGCGAAGAAATGCGCTATGGCTTCGCATATGACACCCGCTGTTTAC 6660
QY 6658 TCACGCTACTAGATACATCCGTTGTGAGAGTCAATCTACCAATGTTGTACTG 6717
Db 6661 TCACGCTACTAGATACATCCGTTGTGAGAGTCAATCTACCAATGTTGTACTG 6720
QY 6718 GCGCCCGAAGCCAGACAGGCGCATAGGTCGTCACAGAGCGGCTTTACATCGGGGCCCC 6777
Db 6721 GCGCCCGAAGCCAGACAGGCGCATAGGTCGTCACAGAGCGGCTTTACATCGGGGCCCC 6780
QY 6778 CTGACTAATCTAAAGGGAGAACTGCGGCTATCGCGGTCGCGGAGCGGTACTG 6837
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Db 6841 ACACACAGCTGCGGTATATCCCTCACATGTTACTTGAAGCGCGCTGCGGCTGTGAGCT 6900
QY 6898 GCGAGCTCCAGGACTGCGAGATGCTGCTATGCGGAGAGAGCTGTGCTATCTGTGA 6957
Db 6901 GCGAGCTCCAGGACTGCGAGATGCTGCTATGCGGAGAGAGCTGTGCTATCTGTGA 6960
QY 6958 AGCGCGGGAGCCACAGAGAGAGAGCGGAGCCTACGCGGCTTCACGGAGCTATGACTGA 7017
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Db 7081 TGCTCTCCAAATGTCACTCGGCGAGATGATGTCGCAAAAGGGTGTACTATCTACCC 7140
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QY 7198 AATTCTGCTAGGACAATCATCATATGATGCGCCACACTTGTGGGCAAGATGATCTGT 7257
Db 7201 AATTCTGCTAGGACAATCATCATATGATGCGCCACACTTGTGGGCAAGATGATCTGT 7260
QY 7258 ATGACATCATTTCTTCTCCATCTCTTACGTCAGAGCAAACTTGAAGAAAGCCCTAGATTGT 7317
Db 7261 ATGACATCATTTCTTCTCCATCTCTTACGTCAGAGCAAACTTGAAGAAAGCCCTAGATTGT 7320
QY 7318 CAGATCTAGCGGCGCTGTTACTACATCTGAGCCACTTACCTCAGATCTTAAGCA 7377
Db 7321 CAGATCTAGCGGCGCTGTTACTACATCTGAGCCACTTACCTCAGATCTTAAGCA 7380
QY 7378 CTCATGCGCTTAGCGCATTTTCTACTCTCATAGTACTCTCCAGGTGAGATCAATAGGGTGT 7437
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QY 7558 TTCACTAGGCGCATAGAGGCAAGCTCAAACTCAGTCCCAATCCCGGCTGCCAGGTG 7617
Db 7561 TTCACTAGGCGCATAGAGGCAAGCTCAAACTCAGTCCCAATCCCGGCTGCCAGGTG 7620
QY 7618 GATTATACAGCTGCTGTCTGCTGCTTACAGCGGGGGAGACATATATACAGCTGTCT 7677
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Db 7621 GATTATACAGCTGCTGTCTGCTGCTTACAGCGGGGAGACATATATACAGCTGTCT 7680
QY 7678 CGTGCCCGAACCCCGCTGCTCATGTGCGCCACTACCTTCTGTAGGGGTAGGCATC 7737
Db 7681 CGTGCCCGAACCCCGCTGCTCATGTGCGCCACTACCTTCTGTAGGGGTAGGCATC 7740
QY 7738 TATCTACTCCCAACCCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGT 7797
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QY 7858 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTCT 7917
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QY 7918 GCGTACCTGTGAAGGTCCGTAGCCGCTTGACTGCAAGAGTCTGATACTGGCTCTC 7977
Db 7921 GCGTACCTGTGAAGGTCCGTAGCCGCTTGACTGCAAGAGTCTGATACTGGCTCTC 7980
QY 7978 TGCAGATCAAGTACT 7992
Db 7981 TGCAGATCAAGTACT 7995

RESULT 14
AAA98967
ID AAA98967 standard; DNA; 8001 bp.
XX
AC AAA98967;
XX
DT 08-FEB-2001 (first entry)
XX
DE Hepatitis C virus DNA fragment SEQ ID NO: 3.
XX
KW Cell culture; therapy; infection; vaccine; diagnosis; gene therapy; ds.
XX
OS Hepatitis C virus.
XX
PN DE19915178-A1.
XX
PD 05-OCT-2000.
XX
PF 03-APR-1999; 99DE-1015178.
XX
PR 03-APR-1999; 99DE-1015178.
XX
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Bartschlagel R;
XX
DR WPI; 2000-629140/61.
XX
PT Cell culture system for hepatitis C virus, useful e.g. in screening for
PT therapeutic agents, comprises human hepatoma cells containing a viral
PT RNA construct that includes a selectable gene -
XX
PS Claim 7: Page 30-36; 58pp; German.
XX
CC This invention describes a novel Hepatitis C virus (HCV) cell culture
CC system comprising human hepatoma cells that contain an integrated HCV-RNA
CC construct (I). (I) contains the HCV-specific RNA segments 5'-NTR
CC (non-translated region), NS (non-structural)1,3, NS4A, NS4B, NS5A, NS5B and
CC 3'-NTR, and a selectable (marker) gene (II). The cell cultures, and/or
CC (I), are used to prepare, evaluate and/or test therapeutic and/or
CC diagnostic agents for HCV infections, and to prepare vaccines against HCV
CC infection (particularly preparation of attenuated HCV). The can also be
CC used for preparation of a liver-specific delivery system for gene
CC therapy, and to identify cells permissive for HCV replication. Virus RNA
CC replicates autonomously and with high efficiency in this cellular system,
CC so that variations in replication rates can be measured (for screening
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QY 2029 ACCAATGTGACACGAGACCTCTGTGGCTGGCAAGCCGCCCCGGGGCGCTTCTTGACA 2088
DB 2041 ACCAATGTGACACGAGACCTCTGTGGCTGGCAAGCCGCCCCGGGGCGCTTCTTGACA 2100
QY 2089 CCATGACACTGCGGAGAGCTGACCTTACTGTGTCACAGAGCATGCGATGTCATTCG 2148
DB 2101 CCATGACACTGCGGAGAGCTGACCTTACTGTGTCACAGAGCATGCGATGTCATTCG 2160
QY 2149 GTGCGCGCGGCGGCGACAGCAGGSGGAGCCTACTCTCCCCAGGCGCTCTCTACTTG 2208
DB 2161 GTGCGCGCGGCGGCGAGACAGCAGGSGGAGCCTACTCTCCCCAGGCGCTCTCTACTTG 2220
QY 2209 AAGGCGCTTGGGGGGGTGCACCTGCTGGCCCTGGGGGACAGCTGTGGGCATCTTTCG 2268
DB 2221 AAGGCGCTTGGGGGGGTGCACCTGCTGGCCCTGGGGGACAGCTGTGGGCATCTTTCG 2280
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DB 2281 GCTGCCGTGTGCACCCGAGGGGTTGCGAAGGCGGTGAGACTTGTACCCGTGAGTCTATG 2340
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DB 2341 GAAACCACTATGCGGTCCCGCGTCTTCACGAGCACTGTCGCCCTCGGCGCTAACGCGAG 2400
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QY 2689 GACTCGACCATATCTCTGGGCAATGCGGCAAGTCTTGACCAAGCGGAGAGCGGCTGAGCG 2748
DB 2701 GACTCGACCATATCTCTGGGCAATGCGGCAAGTCTTGACCAAGCGGAGAGCGGCTGAGCG 2760
QY 2749 GAGCTGCTGTGCTGCGGCGGCTAGCGCTGCGGGATGGGTACCGTCCCATCAGCAAC 2808
DB 2761 GAGCTGCTGTGCTGCGGCGGCTAGCGCTGCGGGATGGGTACCGTCCCATCAGCAAC 2820
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DB 2821 ATGAGAGAGTGGCTCTGTCCAGCACTGAGAAATCCCTTTTATGCAAAAGCCATCCC 2880
QY 2869 ATGAGACCATCAAGGGGGGAGAGCACTCATTTTCTGCCATTCAGAAAGAAATGTGAT 2928
DB 2881 ATGAGACCATCAAGGGGGGAGAGCACTCATTTTCTGCCATTCAGAAAGAAATGTGAT 2940
QY 2929 GAGCTGCGCGGAGAGTGTCCGGCTCGGAGCTCAATGCTGTAGATATTACGGGGCTT 2988
DB 2941 GAGCTGCGCGGAGAGTGTCCGGCTCGGAGCTCAATGCTGTAGATATTACGGGGCTT 3000
QY 2989 GATGTATCCGTCTACCAACTAGCGAGAGCTGATGTGTAGAGCAGCGAGCTCTAATG 3048
DB 3001 GATGTATCCGTCTACCAACTAGCGAGAGCTGATGTGTGTAGAGCAGCGAGCTCTAATG 3060
QY 3049 ACGGGGCTTACCGGGGATTTGAGTCAAGTATGAGTCACTGATATACATGTCACCGAGCA 3108
DB 3061 ACGGGGCTTACCGGGGATTTGAGTCAAGTATGAGTCACTGATATACATGTCACCGAGCA 3120
QY 3109 GTGCACTTCAGGCTGAGCCCGACCTTCACCATGTAGAGAGAGAGCCGTCACAGAGCGG 3168
DB 3121 GTGCACTTCAGGCTGAGCCCGACCTTCACCATGTAGAGAGAGAGCCGTCACAGAGCGG 3180
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DB 3181 GTGTCACGCTGCGAGCGGCGAGGAGAGCTGTAGGGGGAGAGATGGGCATTTACAGGTT 3240
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DB 3241 GTGACTCCAGAGAGAGCGCCCTCGGAGATGTCATGCTCTCGGTGTCGAGTGTAT 3300
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DB 3301 GAGCGGGGCTGTGTTGTAGAGCTACAGCCCGCCGAGACCTTGTAGGTTGCGGCT 3360
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DB 3541 CCATGTTGGGAGCAATGTGAGAGTGTCTATAGGGCTAAAGCTTACGTCAGAGGAGCA 3600
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DB 3601 ACGCCCTGCTGTATAGGCTGGAGCGCTTCAAAAGAGGTTACTACACACACCCATA 3660
QY 3649 ACCAATATCATATGAGCATGTGCGGTACCGTGGAGGTCGTCAGAGAGACCTGGTG 3708
DB 3661 ACCAATATCATATGAGCATGTGCGGTACCGTGGAGGTCGTCAGAGAGACCTGGTG 3720
QY 3709 CTGTTAGGGGAGTCTGTAGCACTCTGCGCGGTATTCCTGACACAGGCGGTGGTC 3768
DB 3721 CTGTTAGGGGAGTCTGTAGCACTCTGCGCGGTATTCCTGACACAGGCGGTGGTC 3780
QY 3769 ATTGTGAGAGATCATCTGTGCGGAGAGCGCGCATCATTTCCGACAGGAGTCTT 3828
DB 3781 ATTGTGAGAGATCATCTGTGCGGAGAGCGCGCATCATTTCCGACAGGAGTCTT 3840
QY 3829 TACGGGAGTTCGATGAGATGGAAGTGGCGTCCACACTCCCTTACATCAGAACAGGA 3888
DB 3841 TACGGGAGTTCGATGAGATGGAAGTGGCGTCCACACTCCCTTACATCAGAACAGGA 3900
QY 3889 ATGCACTGCGGAACATTTCAACAGAGGCAATCGGGTGTCTGCAAAAGCCACCAAG 3948
DB 3901 ATGCACTGCGGAACATTTCAACAGAGGCAATCGGGTGTCTGCAAAAGCCACCAAG 3960
QY 3949 CAAGCGAGAGTGTGCTGCTCCGTTGGTGAATCAGAGTGGCGAGCCCTGGAAGCTTTCG 4008
DB 3961 CAAGCGAGAGTGTGCTGCTCCGTTGGTGAATCAGAGTGGCGAGCCCTGGAAGCTTTCG 4020
QY 4009 GCGAAGCATATGTGAATTTCAATCAGCGGAGATACAAATTTAGCAGGCTTGTCCACTTG 4068
DB 4021 GCGAAGCATATGTGAATTTCAATCAGCGGAGATACAAATTTAGCAGGCTTGTCCACTTG 4080
QY 4069 CCTGGAAACCCCGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4128
DB 4081 CCTGGAAACCCCGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4140
QY 4129 ACCACCAACATACCTCTCTGTTTAAATCTCTGGGGGAGTGGGTGGCGCCCAACTTGCT 4188
DB 4141 ACCACCAACATACCTCTCTGTTTAAATCTCTGGGGGAGTGGGTGGCGCCCAACTTGCT 4200
QY 4189 CCTCCAGAGCTGCTTCTGCTTCTGCTAGGCGCGGCACTGCTGAGAGCGGCTGTTGGAGC 4248
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Dh	4201	CTCTCCAGCCCTTCTTCTCTTCGTAAGCGCGGCATCGCTGAGAGCGCTGTGGCCAGC	4260
QY	4249	ATAGGCCCTTGAGAGGTGCTTGATATTTTGGCAGGTTATGAGACAGGGGTGCGAGCG	4308
Dh	4261	ATAGGCTTGGAGAGTGCCTTGAGATTTTGGCAGAGTTATGAGACAGGGGTGCGAGCG	4320
QY	4309	GGCGTGTGGCCCTTTAAGTGCATGAGAGCGGCGAGTGGCCCTCACCGAGAGACTGGCTAAC	4368
Dh	4321	GGCGTGTGGCCCTTTAAGTGCATGAGAGCGGCGAGTGGCCCTCACCGAGAGACTGGTAAAC	4380
QY	4369	CTACTCCCTCTATTCCTCTCCCTGCGGCCCTAGTCGTGGGGGTCTGTGTGCGACGCATA	4428
Dh	4381	CTACTCCCTCTATTCCTCTCCCTGCGGCCCTAGTCGTGGGGGTCTGTGTGCGACGCATA	4440
QY	4429	CTGTGTGAGACATGGGGCCAGGGGAGGGGGGTGTGAGTGTGATGAACCGGCTGATAGCG	4488
Dh	4441	CTGTGTGAGACATGGGGCCAGGGGAGGGGGGTGTGAGTGTGATGAACCGGCTGATAGCG	4500
QY	4489	TTTCGCTTGGGGGTAAACACAGCTCTCCGCCACGACACTATGTGCTGAGACGACGCTGCA	4548
Dh	4501	TTTCGCTTGGGGGTAAACACAGCTCTCCGCCACGACACTATGTGCTGAGACGACGCTGCA	4560
QY	4549	GCACGTGTCACTAGATTCCTCTCTATCTTACCATCACTCAAGACGTGCTGAAGAGGCTTCAC	4608
Dh	4561	GCACGTGTCACTAGATTCCTCTCTATCTTACCATCACTCAAGACGTGCTGAAGAGGCTTCAC	4620
QY	4609	CAGTGTATCAAGAGGAGCTGTCTCACAGCCATGCTCCGGCTGTGGGTAGAGATGTTTGG	4668
Dh	4621	CAGTGTATCAAGAGGAGCTGTCTCACAGCCATGCTCCGGCTGTGGGTAGAGATGTTTGG	4680
QY	4669	GATTGATATGACACGGGTGTGACTGTATTTCAAGACCTGGTGTCAATCCAACTCTCTCGG	4728
Dh	4681	GATTGATATGACACGGGTGTGACTGTATTTCAAGACCTGGTGTCAATCCAACTCTCTCGG	4740
QY	4729	CGATTGCCGGGAGTCCCTCTTCTTCATGTCAACGTGGGTACAGGGAGTCTGCGGGGCG	4788
Dh	4741	CGATTGCCGGGAGTCCCTCTTCTTCATGTCAACGTGGGTACAGGGAGTCTGCGGGGCG	4800
QY	4789	GACGGCATCATGCAAAACCACTCCCTCATGTGGAGCAGACATACCGGACATGTAAAAAA	4848
Dh	4801	GACGGCATCATGCAAAACCACTCCCTCATGTGGAGCAGACATACCGGACATGTAAAAAA	4860
QY	4849	GGTTCCATGAGAGATCGTGGGGCTTAGGACCTGTAGTACACGTGGCATGGAACATTCCCC	4908
Dh	4861	GGTTCCATGAGAGATCGTGGGGCTTAGGACCTGTAGTACACGTGGCATGGAACATTCCCC	4920
QY	4909	ATTAAACGGTACACACAGGGGCCCTCACGCCCTCCCGGCGCCCAAAATTATTCAGGGCG	4968
Dh	4921	ATTAAACGGTACACACAGGGGCCCTCACGCCCTCCCGGCGCCCAAAATTATTCAGGGCG	4980
QY	4969	CTGTGGCGGGTGTGCTGTAGAGAGTACGTGAGAGTTACCGGGGTGGGGATTTTCACACTAC	5028
Dh	4981	CTGTGGCGGGTGTGCTGTAGAGAGTACGTGAGAGTTACCGGGGTGGGGATTTTCACACTAC	5040
QY	5029	GTGACGGGCATGACACTGTACAACGTAAGATGCCGTGTGACAGTTTCCGGCCCCGAAATTC	5088
Dh	5041	GTGACGGGCATGACACTGTACAACGTAAGATGCCGTGTGACAGTTTCCGGCCCCGAAATTC	5100
QY	5089	TTTCACAGAATGATGGGGGTGGGGTGTGCACAGTACGCTCCACGCTGAACCCCTCTCTA	5148
Dh	5101	TTTCACAGAATGATGGGGGTGGGGTGTGCACAGTACGCTCCACGCTGAACCCCTCTCTA	5160
QY	5149	CGGAGAGAGTCACATTCCTGTGTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCA	5208
Dh	5161	CGGAGAGAGTCACATTCCTGTGTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCA	5220
QY	5209	TGCGAGCCCGAACCAGACGTAGACGTACGTTCATCTCATCCAGACCCCTCCACACTT	5268
Dh	5221	TGCGAGCCCGAACCAGACGTAGACGTACGTTCATCTCATCCAGACCCCTCCACACTT	5280
QY	5269	ACGGGAGAGACGGCTAAGCCTAGCCTAGCGCCAGGGAGTCCGCCCTCTTGTGGCCAGCTCA	5328

Db	5281	ACGGCGAGACGGCTTACGGCTAGGCTAGGCTGGCCAGGGAGTCTCCGCCCTCTTBSGCACGTCA	5340
Qy	5329	TCAGCTAGCCAGCTGTCTGCGCGCTTCTCTTGAAGGCAACATGCATACCCGTATGACTCC	5388
Db	5341	TCAGCTAGCCAGCTGTCTGCGCGCTTCTCTTGAAGGCAACATGCATACCCGTATGACTCC	5400
Qy	5389	CCGAGCGCTAGCTCAATCGAGGGCAACCTCTGTCGGCGCAGAGAAATGGGGGGGAATC	5448
Db	5401	CCGAGCGCTAGCTCAATCGAGGGCAACCTCTCTGTGGCGCAGAGAAATGGGGGGGAATC	5460
Qy	5449	ACCGCGCTGAGTCAGAAAAATAAAGTAGTAATTTTGGACTCTTTGAGCGCGCTCCAAAGC	5508
Db	5461	ACCGCGCTGAGTCAGAAAAATAAAGTAGTAATTTTGGACTCTTTGAGCGCGCTCCAAAGC	5520
Qy	5509	GAGGAGATGAGAGGGGAAGATCCGTTCGGGGGAGATCCTCGGAGATCCAGAAAAATC	5568
Db	5521	GAGGAGATGAGAGGGGAAGATCCGTTCGGGGGAGATCCTCGGAGATCCAGAAAAATC	5580
Qy	5569	CCTCGAGCATGCCCATATGAGGCACCGCCGGATTACAAACCTCCACTGTTAGATCTCTCG	5628
Db	5581	CCTCGAGCATGCCCATATGAGGCACCGCCGGATTACAAACCTCCACTGTTAGATCTCTCG	5640
Qy	5629	AAGGACCCGGAGCTACGTCCTCCAGTGGTACAGGGGTGCATTCCTCCCGCCGACAAAGCC	5688
Db	5641	AAGGACCCGGAGCTACGTCCTCCAGTGGTACAGGGGTGCATTCCTCCCGCCGACAAAGCC	5700
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Db	5701	CCTCGATACCACTCCACGGAGAGAGAGGGTTGTCTCTCAAGATCTACGGTGTCT	5760
Qy	5749	TCCTCCTTGGCGGAGCTCGGCACAAAGACCTTCGGAGCTCCGAATCTCGCGCGTGCAC	5808
Db	5761	TCCTCCTTGGCGGAGCTCGGCACAAAGACCTTCGGAGCTCCGAATCTCGCGCGTGCAC	5820
Qy	5809	AGCGGCAACGGCAAGCGCTCTCTTACACACCTCCAGAGAGGGGAGAGCGGGATCCGAC	5868
Db	5821	AGCGGCAACGGCAAGCGCTCTCTTACACACCTCCAGAGAGGGGAGAGCGGGATCCGAC	5880
Qy	5869	GTTAGTGCATCTCTTCATGCCCCCTTGAGAGGGAGACCAGGGGATCCGATCTCAGC	5928
Db	5881	GTTAGTGCATCTCTTCATGCCCCCTTGAGAGGGAGACCAGGGGATCCGATCTCAGC	5940
Qy	5929	GAGCGGCTTGTCTTACCCTGTAAGCGAGAGAGCTAGTGAAGAGTGTGTGCTGCTCGATG	5988
Db	5941	GAGCGGCTTGTGTCTTACCCTGTAAGCGAGAGAGCTAGTGAAGAGTGTGTGCTGCTCGATG	6000
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Db	6061	ATCATAGCACTGAGACCACTTTTGTGTCGCGACACCAATGTGTATCTTCAACATCT	6120
Qy	6109	CGCAGCGCAAGCTTGCGGCGAAGAAAGTCACTTTGACAGACTGCAAGTCTCTGCAAGAC	6168
Db	6121	CGCAGCGCAAGCTTGCGGCGAAGAAAGTCACTTTGACAGACTGCAAGTCTCTGCAAGAC	6180
Qy	6169	CACATACGGGAGCGTCTCAAGAGATGAAGAGCAAGCGCTCCACATTTAAGCTTAACTT	6228
Db	6181	CACATACGGGAGCGTCTCAAGAGATGAAGAGCAAGCGCTCCACATTTAAGCTTAACTT	6240
Qy	6229	CTATCCGTGAGGAAGCCTGTAAAGCTGACGCCCCCACTTGGCCAGATCTAAATTTGGC	6288
Db	6241	CTATCCGTGAGGAAGCCTGTAAAGCTGACGCCCCCACTTGGCCAGATCTAAATTTGGC	6300
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 Db 6601 TTCTGTGATGATGCTGGAAGCGAAGAAATGCCCTATGGGCTTGCAATATACACCGC 6660
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 Db 6721 TGTACTTTGGCCCGAGACAGACAGGCCATAGGTCGCTCACAGAGCGGCTTTACATC 6780
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 Db 6781 GGGGGCCCCCTGACTAATTTCTAAAGGCGAGACTGCGGCTATGCCGCTGCGCGAGC 6840
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 Db 7441 AATAGGGTGGCTTCAATGCTCAGAGAACTTGGGGTACCGCCCTTGGAGTCTGGAGACAT 7500

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 Db 7681 AGCCTGTCTGTGCCGACCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7740
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 Db 7801 CCATCTGT 7860
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 Db 7921 CCTAGTACAGGCTAGCTGTGAAGGTCCGTGAGCCGCTTGCATGACAGAGTGTGATAC 7980
 QY 7969 TGGCCTCTCTGCAATCAAGT 7989
 Db 7981 TGGCCTCTCTGCAATCAAGT 8001

RESULT 15
 AAD25323
 ID AAD25323 standard; cDNA; 7846 BP.
 AC AAD25323:
 DT 12-Mar-2002 (first entry)
 DE Hepatitis C virus (HCV) adaptive replicon I cDNA mutant.
 KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
 adaptive replicon I; mutant; ss.
 OS Hepatitis C virus.
 XX Synthetic.
 XX key Location/Qualifiers
 FH 4642..5841
 FT CDS
 FT /*tag- a
 FT /product= "NS5A protein of HCV adaptive replicon I"
 FT /note= "CDS does not include both start and stop
 codon"
 FT /partial
 XX
 XX W0200189364-A2.
 XX
 XX 29-NOV-2001.
 XX
 XX 23-MAY-2001; 2001WO-US16822.
 XX
 XX 23-MAY-2000; 2000US-0576989.
 XX
 XX (UNIW) UNIV WASHINGTON.
 XX
 XX Rice CM, Blight KJ;

XX WPI: 2002-066755/09.
DR P-PSDB: AAE15719.

XX Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences

PS Claim 17, page 72-74; 174pp; English.

XX The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets,
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficiency replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays,
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated or defective HCV derivatives for expression of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) adaptive replicon I cDNA mutant. This sequence
CC is generated by the deletion of nt 5345-5485 of HCVrepBattman/Avair
CC cDNA.

XX Sequence 7848 BP; 1614 A; 2328 C; 2202 G; 1704 T; 0 other;

XX Query Match 96.2%; Score 7689; DB 24; Length 7848;

XX Best Local Similarity 98.2%; Pred. No. 0;

XX Matches 7843; Conservative 0; Mismatches 5; Indels 141; Gaps 1;

QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACCATAGATACCTCCCTGTGAGAACTACTG 60
DB 1 GCCAGCCCCCGATTGGGGGCGACACTCCACCATAGATACCTCCCTGTGAGAACTACTG 60
QY 1 TCTTCACGAGAAAGCGTGTACCATGGGAGTATGATAGTGTGAGAGCTCCAGAC 120
DB 1 TCTTCACGAGAAAGCGTGTACCATGGGAGTATGATAGTGTGAGAGCTCCAGAC 120
QY 1 TCTTCACGAGAAAGCGTGTACCATGGGAGTATGATAGTGTGAGAGCTCCAGAC 120
DB 1 TCTTCACGAGAAAGCGTGTACCATGGGAGTATGATAGTGTGAGAGCTCCAGAC 120
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DB 361 CTCAGAGAAACCAAGGCGCGCATGATGTAACAGATGATGATGACGACGATGCTC 420
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DB 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGGGCAACAAGACATGCGTGTCT 480
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DB 481 CTGATGCGCGGTGTCCGCTGTCAGGCGGAGGCGCGGCTTTTGTGAACAGCG 540
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DB 541 ACCTGTCCGGTCCCTGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
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DB 601 CGAGGGGGCTTCTTGGCGGAGCTGTGCTGACGAGGAGGAGGAGGAGGAGGAGGAGG 660
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DB 841 TTGTGATCAGATATGATGACGAGGAGCATGAGGGGCTCGGCGGAGGAGGAGTGTG 900
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DB 961 GCTTCGCGATATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
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DB 1021 TGGGATGCGGAGCGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
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DB 1141 AGCGATGCGCTTCTATGAGGCTTCTTGAAGGATCTTGTGAAGTAAACAGACACAG 1200
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DB 1321 CCGTCTTTGGCAATGTAAGGCGCGGAACCTGCTCTTCTTGAAGAGGATTCCT 1380
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DB 1381 AGGGGCTTTCCTCTGCGGCAAGGAGTGAAGTGTGAATGCTGAAGAGGAGCA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGAGCAACAGTGTGAGGAGCCTTTGACAGGACGG 1500
DB 1441 GTTCTCTGGAAGCTTCTTGAAGAGCAACAGTGTGAGGAGCCTTTGACAGGACGG 1500


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Job time : 1019 secs

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Db 4796 GCAAGGGGAGAGCAATGTTAGGGGAGAGTGGGATTTACAGGTTGTGACTCAG 4855

Qy 3240 AGAAGGCCCTCGGAGATTTGATTCCTCGGTTCTGTGCAAGTCTATGACGGGGCTG 3299
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Db 4916 TGCTTGTATGACTACGCGCGGAGACCTCACTTATAGTTGGGGCTTACTTAACAC 4975
Qy 3360 ACCAGGTTCCCGTCTGCGAGACCATGTGAGTTCTGGAGAGCGTCTTACAGGCT 3419
Db 4976 ACCAGGTTCCCGTCTGCGAGACCATGTGAGTTCTGGAGAGCGTCTTACAGGCT 5035
Qy 3420 CACCCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGAGAGCAACTTCCCTA 3479
Db 5036 CACCCACATAGATGGCCACCTCTGTGCCAGACTAAGCAGGAGAGCAACTTCCCTA 5095
Qy 3480 CTTGTAGCATACAGGCTACGAGTGTGCGCCAGGGCTGAGGCTCCACCTCATGAGGA 3539
Db 5096 CTTGTAGCATATCAAGCTACAGTGTGCGCCAGGGCTCAAGCTCCACCTCATGAGGA 5155
Qy 3540 CCAATGTGAGAGTGTCTATACGAGTAAAGCTTACGCTGCAAGGCGCAAGCCCTGCT 3599
Db 5156 CCAATGTGAGAGTGTCTATACGAGTAAAGCTTACGCTGCAAGGCGCAAGCCCTGCT 5215
Qy 3600 GTATAGGCTGGAGCGGCTTCAAAACGAGGTTACTACACACACCCCATACCAATACAT 3659
Db 5216 GTATAGGCTGGAGCGGCTTCAAAATAGGTCATCTCCACACACCCCATACCAATACAT 5275
Qy 3660 CATGCAATGATGTGCGCTGACCTGAGGTGCTTACAGACACCTGGGTGCTGTAGGCGG 3719
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Qy 3720 AGTCTGACAGCTGTGCGCGCTATGCTGAGCAAGAGCAGCAGTGTATGTGGGAG 3779
Db 5336 AGTCTGACAGCTGTGCGCGCTATGCTGAGCAAGAGCAGCAGTGTATGTGGGAG 5395
Qy 3780 GATCATCTTGTCCGGAAGCGCGCATCATTCGCGACAGGAAATGCTTACCGGAGTT 3839
Db 5396 GATCATCTTGTCCGGAAGCGCGCATCATTCGCGACAGGAAATGCTTACCGGAGTT 5455
Qy 3840 CGATGAGATGAGAGAGTGGCGCTCACAGCTCCCTTACATGCAAGAGGAATGACCTGCG 3899
Db 5456 CGATGAGATGAGAGAGTGGCGCTCACAGCTCCCTTACATGCAAGAGGAATGACCTGCG 5515
Qy 3900 CGAACATTTCAACAGAGGCAATCGGGTTGCTGCAAGACGCCACCAAGCGAGGCG 3959
Db 5516 CGAACATTTCAAGCAAAAGCGCTCGGGTTGTGCAAAAGCGCCACCAAGCGAGGCG 5575
Qy 3960 TGTGCTCCCGGTGGAAATGCAAGTGGCGGAGCCCTGCAAGCCCTTGGGGAGATAT 4019
Db 5576 TGTGCTCCCGGTGGAGTCCAAAGTGGAGCCCTTGAAGACCTTGTGGCGAAGACAT 5635
Qy 4020 GTGAATTTATCAGCGGAGTACAAATATTAGCAGGCTTGTCACTCTGCTGCAAGCC 4079
Db 5636 GTGAATTTATCAGCGGAGTACAAATATTAGCAGGCTTGTCACTCTGCTGCAAGCC 5695
Qy 4080 CGCATATGATCACTGATGAGCATTTACAGGCTTATACAGCGCGCTACCAACCAACA 4139
Db 5696 CGCATATGATCACTGATGAGCATTTACAGGCTTATACAGCGCGCTACCAACCAACA 5755
Qy 4140 TACCTCCTGTTTACATTCCTGGGGGATGAGTGGCGGCCCACTTGTCTCCAGCGC 4199
Db 5756 CACCTCCTGTTTACATTCCTGGGGGATGAGTGGCGGCCCACTCCTCCAGCGC 5815
Qy 4200 TGCTTCTGCTTCTGAGGCGCGGATCGTGGAGGGGCTGTGGAGATAGGCTTGG 4259
Db 5816 TGCTTCTGCTTCTGAGGCGCGGATCGTGGAGGGGCTGTGGAGATAGGCTTGG 5875
Qy 4260 GAAAGTGTGTGATATTTTGGAGGTTATGAGAGAGGGGTGCAAGGCGGCTGTGCG 4319
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QY	4320	CTTTAAGTCATATAGCGGGAGATGCTCCCTCCACCGAGAACTGGCTAACCTACTCTCCTGC	4379
Db	5936	CTTTAAGTCATATAGCGGGAGATGCTCCCTCCACCGAGAACTGGCTAACCTACTCTCCTGC	5995
QY	4380	TATCCTCTCCCTGGCGCCCTATGTCGCGGGGTCTGTGCGCAGAGAACTAGCTCGTCGGCA	4439
Db	5996	CATCCTCTCTCTGTGTCCTGGTTCGTGCGGGTCTGTGCGCAGAACTAGCTCGTCGGCA	6055
QY	4440	CTGTGCGCCAGGGAGGGGAGCTGTGCACTGGATGTAACCGGCTGATAGCTTGCCTTCGGC	4499
Db	6056	CGTGGCGCCGGGAGAGGGGAGCTGTGCACTGGATGTAACCGGCTGATAGCTTGCCTTCGGC	6115
QY	4500	GGGTAAACACAGTGTCCCGCCACGACTATGTGCTAGAGCGGAGCTGAGCACTGTGCAC	4559
Db	6116	GGGTAAACACAGTGTCCCGCTTACGACTATGTGCTAGAGCGGAGCTGAGCACTGTGCAC	6175
QY	4560	TCAGATCCTCTAGTCTTACATCACTAGCTAGCTGTGAAGAGCTTCACAGTGGATCAA	4619
Db	6176	TCAGATCCTCTAGCTTACATCACTAGCTAGCTGTGAAGAGGCTTCACAGTGGATCAA	6235
QY	4620	CGAGAGATGCTCCACGCAATGCTCCGGCTGTGGGTATAGAGATGTTGGAGTTGGATATG	4679
Db	6236	TGAGAGATGCTCTACGCAATGCTCCGGCTGTGGGTATAGAGATGTTGGAGTTGGATATG	6295
QY	4680	CACGGTTTACTGATTTCAAGACCTGAGCTCCAGTCCAAAGCTCCTGCCGCAATTGCCGG	4739
Db	6296	CACGGTTTACTGACTTCAAGACCTGAGCTCCAGTCCAAAGCTCCTGCCGCGATTACGGG	6355
QY	4740	AGTCCCTTCTTCTCATGTCACTGACGTGGGTACAAGGAGTCTGTGCGGGCGACGGCATCAT	4799
Db	6356	AGTCCCTTCTCTGTCAATGCCACMGCGGGTACAAGGAGTCTGTGCGGGCGACGGCATCAT	6415
QY	4800	GCAACACACCTGGCCATGTGGAGCACAGATATCAACGGACATGTGAAGAAAGATTCCATAG	4859
Db	6416	GCAACACCACTGCCATGTGGAGCACAGATATCCCGGACATGTGAAGAAAGATTCCATAG	6475
QY	4860	GATCGTGGGCGCTTAGCACTGTAGTAACAGTGGCATGGACATTCCCATTTAAACGGTA	4919
Db	6476	GATCGTAGGGCGCTAGAACCTGTGACAGCAACAGTGGCACGGAAGTTCCCATTAACGCGTA	6535
QY	4920	CACACAGGGCGCCCGACAGGCGCTCCCGGGGCGCAATTATTTAGGGGGGTGGGCGGT	4979
Db	6536	CACACAGGAGCTTGTCAACACCTTCCCGGGGCGCAATTATTCAGAGGCGCTATGGCGGT	6555
QY	4980	GGCTGTGAGAGATCACTGTGAGGTTACGGGGTGGGGGATTTCCACTACGTACGAGGGCAT	5039
Db	6596	GGCTGTGAGAGATCACTGTGAGGTTACGGGTGGGGGATTTCCACTACGTACGAGGGCAT	6655
QY	5040	GACCACTGACAACTAAAGTCCCCGTGTAGGTTCCGGCCCCCGAATTCTTACAGAAAT	5099
Db	6656	GACCACTGACAACTAAAGTCCCCATGTGCCAGGTTCCGGCCCCCGAATTCTTACAGGAAT	6715
QY	5100	GGATGGGGTGGGTTGGACAGGTAACCTCCAGGTCGAACACCTCTCTACGGGAGAGAGT	5159
Db	6716	GGATGGAGTGGGTTGGACAGGTAACGCTCCGGGTGTCAACACTCTTTACAGGAGAGAGT	6775
QY	5160	CACATTCCTGTGCGGCTCAATCAATACCTGTTGGGTACAGCTTCCATGTGACCCGA	5219
Db	6776	CACGTTTCAAGTTCGGGCTCAACCAAAATTTGGTGGGTGTGACGCTTCCATGTGAAACCCGA	6835
QY	5220	ACCGAGCTATCACTGTCTCACTTCATGTGCACCGGACCCCTCCACATTAGGGCGGAGAC	5279
Db	6836	ACCGAGCTATCACTGTCTTACTTCCATGCTCACCGATCCCTTCCCATTAACGAGAGAGAC	6895
QY	5280	GGCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTTGGCCAGCTCATACGTTAGCCA	5339
Db	6896	GGCTAAGCGTAGGCTGGCTAGAGGGTCTCCCGCTCTTAGCACACTCATACGTTAGCCA	6955
QY	5340	GCTGTCTGCGGCTTCTTGAAGGCAACATGCACTACCGCTCAATGACTCCCGGAGCGTGA	5399
Db	6956	GTTGTCTGCGGCTTCTTGAAGGCAATGCACTACCGCACTATGACTCCCGGAGCGTGA	7015
QY	5400	CCTATCTCAGGCGCAACCTCTGTGTGGCGGAGAGATGGCGGGGAACATCACCCGCTGGA	5459

Db	7016	CCTATGAGGCCAACCCTCTTGTGGCGGAGAGATGGCGGAAACATCATCCGCTGCA	7075
Qy	5460	GTCAAAATTAAGTAGTATTTTGGACHTTTTCAGAGCCGCTCCAAGCGAGAGATGA	5519
Db	7076	GTCAAGAAATTAAGTAGTATTTCTTGACACTTTTCACACCGCTTCACGGGAGGAGATGA	7135
Qy	5520	GAGGAGTAGTATCCGTTCCGCGGAGATCCTGGGAGAGTCCAGAAATTCCCTCGAGGAT	5579
Db	7136	GAGGAGATATTCGTGCGCGGAGATCTGGAAATCCAGAAATTCCCTCGAGCTT	7195
Qy	5580	GCCCATTTGGGACGCCCGGATTTACCACTCCACTGTTAGAGTCTTGAAGGACCGGA	5639
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Qy	5640	CTACGTCCTTCACAGTGTACACGGGTGTCATTGCCGCTGCGCAAGGCCCTCCGATACC	5699
Db	7296	CTACGTCCTTCACAGTGTATACAGAAAGGCCATTGACACTACCAAGGCTCCTCAATACC	7315
Qy	5700	ACCTCCACGGAGAGAGAGAGCGGTTGCTCCGTACAGATCTACCGTGTTCGCTTGGC	5759
Db	7316	ACCTCCACGGAGAGAGAGAGCGGTTCTCTGACAGATCATATGTTGTTTCTGCTTGGC	7375
Qy	5760	GGAAGCTGCCACAAGAAGCTTGTGGCAGCTCCGATGTCGTGGCGCTGACAGCGCACGCG	5819
Db	7376	GGAGCTGCGCCACTAGACCTTCCTGCTGCTCCGATGCTGGCGCTGTATACGGGACGC	7435
Qy	5820	AAGGCTCTCTGACACAGCCCTCCAGACAGCGGACCGGATCCGAGTTGAGTGTA	5879
Db	7436	GACGCGCTTCTCTACCTGGCTCCGACGACGGTGCACAAAGGATCCGAGTTGATGCTGA	7495
Qy	5880	CTCCCTCATGCCCCCTTTAGGGGAGAGCGCGGAGATCCCGATCTCACGACGAGCTTG	5939
Db	7496	CTCCCTCATGCCCCCTTTGAAGGGAGCGCGGAGGCCCGGATCTCACGACGAGCTTG	7555
Qy	5940	GTTACCGTAGAGAGAGAGGCTAGTAGAGATCTGCTGCTCTCTGATGTCCTACACATG	5999
Db	7556	GTTACCGTAGAGAGAGAGGCTAGTAGAGATCTGCTGCTCTCTGATGTCCTACACATG	7615
Qy	6000	GACAGCGCCCTGATACGCGCATGCGCTCGGAGGAAACAAGCTGCCCATCAATGCACT	6059
Db	7616	GACAGCGCCCTGATACGCGCATGCGCTCGGAGGAAATAAGTGTGCCATCAACCCGTT	7675
Qy	6060	GAGCACTCTTGTCCGTACCAACAATTGGTCTATGCTAACAAATCTCGACGCGCAG	6119
Db	7676	GAGCACTCTTGTCCGTACCAACAATTGGTCTATGCTAACAAATCTCGGAGGCGAG	7735
Qy	6120	CCTGGGAGAGAGAGAGTCACTTTTGACAGACTGCGAGTCTCGAGCAACACTACCGGA	6179
Db	7736	CCTGGGAGAGAGAGAGTCACTTTTGACAGATTTGCAAGTCTCGAGTCAATACCGGA	7795
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Db	7916	GGAGCTCCGGAACCTTATCCAGAGGCGGTTAACCAACATCCGCTCCGTGTGAAGACTT	7975
Qy	6360	GCTGGAAGACACTAGACACCATTGACACACACATCATGGGAAATAATGAGCTTCTG	6419
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Qy	6420	CGTCCAAACAGAGAGAGGCGGCGCAAGCGCTCCCTTATCGATTCCAGATTGGG	6479
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Db 8276 AACGCTACATGAGATGAATCGCTGTGAGAGTCAATCTCAATGTGTGACTTGGC 8335
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Db 8336 CCCCAGAGCCAGACAGCCATAGTGTCTCAGACAGCGGCTTTACATCGGGGGCCCT 8395
QY 6780 GACTAATTTAAAGGCGAGACAGTGGGCTATGCGGGTCCGCGGAGCGGCTGTACTGAC 6839
Db 8396 GACTAATTTAAAGGCGAGACAGTGGGCTATGCGGGTCCGCGGAGCGGCTGTACTGAC 8455
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QY 7260 GACTCATTTTCTTCATCTCTTACTAGAGAACACTTGA AAAAGCCCTAGATTGTCA 7319
Db 8876 GACTCATTTTCTTCATCTCTTACTAGAGAACACTTGA AAAAGCCCTAGATTGTCA 8935
QY 7320 GATCTAGGCGGCTGTACTACATTCATGAGCCACTTGAACCTGATCATTCAGACGAT 7379
Db 8936 GATCTAGGCGGCTGTACTACATTCATGAGCCACTTGAACCTGATCATTCAGACGAT 8995
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QY 7620 TTATCCAGCTGTTGCTGTGCTGTGTTACAGCGGGGAGACATATATCAGACCTGTCTCG 7679
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Db 9296 TGCCGACCCCGCTGTGCTGTGCTGTGTTACAGCGGGGAGACATATATCAGACCTGTCTCG 9355
QY 7740 TCTACTGCCCAACCGATGAGACGGGAGGCTAAACATCCAGGCGCAATAGGCACTGCTT 7799
Db 9356 CTGTGTGCTGTGCTGTGCTGTGTTACAGCGGGGAGACATATATCAGACCTGTCTCG 9405
QY 7800 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 7859
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QY 7860 TTTTCTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 9525
Db 9466 TCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 9585
QY 7920 CTAGCTGTAAAGTCTGAGCGCTGTGAGCTGAGAGAGTGTGATGATGAGCTGTCTG 7979
Db 9526 CTAGCTGTAAAGTCTGAGCGCTGTGAGCTGAGAGAGTGTGATGATGAGCTGTCTG 9585
QY 7980 CAGATCAATG 7989
Db 9586 CAGATCAATG 9595

RESULT 2
US-08-324-977-31
Sequence 31, Application US/08324977
Patient No 5747339
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKU, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McIreland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996

FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 7917 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA from genomic RNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7862
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..7916
OTHER INFORMATION: /note="sequence = 1500 - 9416 of
OTHER INFORMATION: SEQ ID NO: 1"
US-08-324-977-31

Query Match 65.3%; Score 5218; DB 1; Length 7917;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;

QY 1800 CATGGCGCTATTACGGCTACTGCTCCCAACAGACGCGAGGCGCTACTGGCTGCATCTAC 1859
DB 1908 CCTGGGCCCATACGCGGCTACTGCTCCCAACAGACGCGGCGCTACTGGCTGCATCTAC 1967
QY 1860 TAGCCTCAACAGCGCGGAGACAGCAAGTGTGAGGGGAGAGTCCAGGTGTCTCCACCGC 1919
DB 1968 TAGCTTCAACAGCGCGGAGACAGCAAGTGTGAGGGGAGAGTCCAGGTGTCTCCACCGC 2027
QY 1920 AACCAATCTTCTGCGACGCTGCGTCAATGCGCTGTGTGAGTGTATCATGTGTC 1979
DB 2028 AACCAATCTTCTGCGACGCTGCGTCAATGCGCTGTGTGAGTGTATCATGTGTC 2087
QY 1980 CGGCTCAAGACCTTCCGCGCCCAAGGCGCCCAATCCCAATGTACCAATGTGGA 2039
DB 2088 TGGCTCAAGACCTTCCGCGCCCAAGGCGCCCAATCCCAATGTACCAATGTGGA 2147
QY 2040 CCAGGACCTGCTGCGTGGGCAAGGCGCGCGCGGCGCTTCTTACACCATGACACCTG 2099
DB 2148 CCAGGACCTGCTGCGTGGGCAAGGCGCGCGCGGCGCTTCTTACACCATGACACCTG 2207
QY 2100 CGGAGCTCGACCTTACTTGTGTACAGAGCATGCGCATGATTCGGGTGCGCGGCG 2159
DB 2208 TGGAGCTCGACCTTACTTGTGTGTACAGAGCATGCTGATGCTATTCGGGTGCGCGG 2267
QY 2160 GGGGACAGCAGGGGGAGGCTACTTCTGCGCCAGGCGCGTCTCTACTTGAAGGGCTCTTC 2219
DB 2268 GGGGACAGCAGGGGGAGGCTACTTCTGCGCCAGGCGCGTCTCTACTTGAAGGGCTCTTC 2327
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DB 2328 GGGGAGTCCACTGCTGTGCGCTTTCGGGAGCGGTGTGAGGATCTTTCGGGCTGCGCTGTG 2387
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DB 2448 GCGGTCCCGGTTCTTACAGGACATCGTCCCTCCGCGGATACCGGACATTCAGAGT 2507

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DB 2508 GGCCCATCTTACAGCCCGCTACTGTAGGGCAAGAGCACTAAGTGTGCGGTATGCT 2567
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QY 2760 GCTGGCACCGCTACCGCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGAGGT 2819
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QY 2820 GGGTCTCTCAGACATGGAATCCCTTTTGGCAAGGATCCCATGAGAGCAT 2879
DB 2928 GGGTCTCTCAGACATGGAATCCCTTTTGGCAAGGATCCCATGAGAGCAT 2987
QY 2880 CAAGGGGGAGAGGACCTCATTTTCTGCCATTCCAGAAATGTATGAGTGCCTG 2939
DB 2988 CAGGGGGAGAGGATGATCTTTCTGTCTCCAGAAATGTATGAGTGCCTG 3047
QY 2940 GAAGCTGTCCGGCTCGGACTCAATGTGTAGCATTTACCGGGGCTGTATGCTGCT 2999
DB 3048 AAAGCTGTCCGGCTCGGACTCAATGTGTAGCATTTACCGGGGCTGTATGCTGCT 3107
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DB 3108 CATACACACTAGCGGACGCTCATTTGTGAGCAAGGAGCGCTATGAGCGGCTTTAC 3167
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DB 3228 CTTGGATCCGACCTTGTACATGTAGAGAGAGAGCGGCTGCAAGAGCGGCTGACGCTC 3287
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DB 3288 GCAAGCGGAG 3347
QY 3240 AGAAGGCGGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3299
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RESULT 3
US-08-384-616-31
Sequence 31, Application US/08384616
Patent No. 5847101
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, McDaniel &
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384, 616
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769, 996
FILING DATE: 02-OCT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635, 451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 7917 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..7862
NAME/KEY: misc_feature
LOCATION: 1..7916
OTHER INFORMATION: /note="sequence = 1500 - 9416 of
OTHER INFORMATION: SEQ ID NO: 1"
US-08-384-616-31
Query Match 65.3%; Score 5218; DB 2; Length 7917;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;

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Db	3588	CCTGTTAGCATACCAAGGCTACGGGTGGGCGGAGGGCTCACACCTCCATCGTGGGA	3647
Qy	3540	CCAAATGTGAAGTGTCTCATAGGCTAAGCCTACGCTGCACAGGGCCAAAGCCCTGCT	3599
Db	3648	TCAATGTGAAGTGTCTCATAGGCTAAGCCTACGCTGCACAGGGCCAAAGCCCTGCT	3707
Qy	3600	GTAATAGGTGGGAGCCGTTCAAAACAGAGTTACTACCACACACCCCATACCAATTACT	3655
Db	3708	GTAACGGGTGGGAGCCGTTCAAGATGAGGTCACCTCCACCCACCCCATACCAAAATTACT	3767
Qy	3660	CATGGCATGATGTTCGGGCTACCTGAGAGTGTGTACAGAGACACTGGGTCTGTAGGGG	3719
Db	3768	CATGGCATGATGTTCGGGCTACCTGAGAGTGTGTGTACAGAGACACTGGGTCTGTAGGGG	3827
Qy	3720	AGTCTTAGCAGCTTGGCCGCGATTTGCTGTACAAACAGGACGCTGTATTGTGGCAG	3779
Db	3828	AGTCTTTGACACTGTGGCCGCGATTTGCTGTACAAACAGGAGAGTGTATTGTGGGAG	3887
Qy	3780	GATCAATCTTGCAGGAAGGCGGCAATCATTTCCGACAGGGAAGTCTTTACCGGAGAT	3839
Db	3888	GATTAATCTTGTCCGGAGGCGGCAATTTGTTCCGACAGGAGCTTCTTACCAGAGAT	3947
Qy	3840	CGATGAGATGGAAGTGGCGCTCACACTCCCTTACATGAAACAGGAATGACACTGCG	3899
Db	3948	CGATGAATATGGAAGTGGCGCTGCGACTCCCTTACATGAAACAGGAATGACACTGCG	4007
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Db	4008	CGAGCAATTTCAAAGGAAGGCGCTGGGTTACTGTCAAAACGCCACCAACAGCGGAGGC	4067
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Db	4128	GTGGAATTTTCATAGCGGGATACAGTACTTACCAAGCTTATCCACTCTGCTGGGAACC	4187
Qy	4080	CGGATAGCACTGATGTGGCAATTCACACGCTCTTACACAGCCCGCTCACACCCACA	4139
Db	4188	CGCATAGCACTGTGTGGCAATTCACACGCTCTTACACAGCCCGCTCACACCCACAAG	4247
Qy	4140	TACCCCTCTGTTTACATCCTGTGGGGGATGGGTGGCCGCCCAACTTGTCTCCACAGC	4199
Db	4248	TACCCCTCTGTTTACATCTTGGGGGGTGGGTGGGTGCCCAACTGCCCCCACAAGC	4307
Qy	4200	TGCTTTGCTTTCGTGTAGGCGCCGGGCAATCGCTGAGCGGCTGTGGACCATAGGCCCTTGG	4259
Db	4308	CGCTTCGAGCTTGTGTGGCGCCCGGCAATCGCCGGTGGGTGTGGCAACATAGGCTTGG	4367
Qy	4260	GAAAGTCTGTGGATATTTTGTGCAGATTATGAGCAGAGGCTGGCAGAGCGGCTGTGGC	4319
Db	4368	GAAAGTCTGTGTGACATTTGTGGCGGGTTATGGAGCAGAGGCTGGCAGAGCGGCTGTGGC	4427
Qy	4320	CTTTAAGTCAATGACGGGGAGATGCCCTTCACCCAGGACCTGGCTAACTTACTCTTCG	4379
Db	4428	CTTTAAGTCAATGACGGCGAGATGCCCTTCACCCAGGACCTGGCTAACTTCTTCGCG	4487
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Db	4488	CATCCTCTCTCTGTGGCGCCCTTGGTCTCGGGGTCTGTGTGTGACGCAATTTCTCGTCACA	4547
Qy	4440	CGTGGGCCACAGGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTCTGCTCGG	4489
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Qy	4500	GGGTAAACCACTCTCCCCACAGCAATATGGCTGTGAGCGAGCGCTGACAGCACTGTAC	4559
Db	4608	GGGTAACTATGTTTCCCCACAGCACTATGTGCTGTGAGCGAGCGCGCAGCGCTGTAC	4667
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Qy	4680	CACGCTGTGACTATTTCAAGACCTGTGCACAGTCCCAAGCTCTCGCGCACTTCCCGG	4739
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Qy	4920	CACCAAGGCCCCCTGACAGCGCTTCCCGGGGCCAAATTTCTAAGGGCGCTTGGCGGT	4979
Db	5028	CACCAAGGCCCCCTGACACACCTCTCCAGGGCCAAACTATTTCTAAGGGCGCTTGGCGGT	5087
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APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: McEland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 9007036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 7917 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
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NAME/KEY: CDS
LOCATION: 1..7862
FEATURE:
NAME/KEY: misc-feature
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QY 1860 TACCTCTACAGGCGCGGACAGAACAGAGTGCAGGGGGAGGTCAGAGTGCTTCCACCGC 1919
Db 1968 TACCCTTACAGGCGGGGACAGAACAGACAGAGTGCAGGGAGAGAGTTCAGGTTCACACGC 2027
QY 1920 AACACATCTTTTCTGGGCACTGGGTCAATAGCGCTGTGTGACATCATATCATATGTC 1979
Db 2028 AACACATCTTTTCTGGGCACTGGGTCAATAGCGCTGTGTGACATCATATCATATGTC 2087
QY 1980 CGGCTCAAGACCTTGGCGGCGCCAAAGAGGCCAATCACCCAAATGTACACCAATGTGA 2039
Db 2088 TGGCTCAAGACCTTGGCGGCGCCAAAGAGGCCAATCACCCAGATGTACACCAATGTGA 2147
QY 2040 CCAAGACTGTGCTGGTGCAGAGCGCCCCCGGGGCGGCTTCTTGACACCATGCACTTG 2099
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OY	2280	CACCCGAGGG	GTG	CCAAAGG	CGGTG	AGCTTTG	TAC	CCCTCG	AGTCT	ATG	AAACCA	CTAT	2339		
Db	2388	CACCCGGGGG	GTG	CCAAAGG	CGGTG	AGCTTTG	TAC	CCCTCG	AGTCT	ATG	AAACCA	CTAT	2447		
OY	2340	GGGGTCCCGG	TTT	TACG	GAACAC	TCGTC	CCCTCG	CGG	CTTAC	CGG	AGCAT	CCAGG	2359		
Db	2448	GGGGTCCCGG	TTT	TACG	GAACAC	TCGTC	CCCTCG	CGG	CTTAC	CGG	AGCAT	CCAGG	2507		
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Db	2508	GGCCCATCT	ACACG	CCCTACT	GTGTAG	CGGCA	AGCACT	AAAGT	GCCG	GCCTG	CGTAT	ATG	2567		
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OY	2580	CACCAAGGG	ATG	CCCCC	ATC	ACG	TAC	CACTCA	CACTAT	GTG	CAAG	TTT	CTTG	CG	2639
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OY	2640	CTCTGGGGGG	CCCTAT	ATG	CACTAT	TAT	TAT	GTATG	ATG	TC	CACT	TAC	TACT	G	2699
Db	2748	CTCTGGGGGG	CCCTAT	ATG	CACTAT	TAT	TAT	GTATG	ATG	TC	CACT	TAC	TACT	G	2807
OY	2740	TATCTGGG	GCAT	TCGG	CACT	CTCT	TG	ACCAAG	CGG	AG	CGG	CTG	TG	AG	2759
Db	2808	AATCTGGG	GCAT	TGGC	CACT	CTCT	TG	ACCAAG	CGG	AG	CGG	CTG	TG	AG	2867
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Db	2868	GCTGGCAC	CGCT	TAC	GCCT	CTCG	GGAT	TCGG	TAC	CGCT	GC	CAC	TCC	AA	2927
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Db	2928	GGCTCTGT	CCAG	CACTG	AG	AAAA	TCC	CCCTTT	AT	GG	CA	AG	CCAT	CC	2987
OY	2880	CAAGGGGGG	AG	GGAC	CTCAT	TTT	CT	GCAT	TCC	AA	GA	AA	TG	T	2939
Db	2988	CAAGGGGGG	AG	GGAC	CTCAT	TTT	CT	GCAT	TCC	AA	GA	AA	TG	T	3047
OY	2940	GAAAGTGT	CCGG	CCCTCG	AG	ACTAT	GTG	TAG	CACTAT	T	T	CC	GG	CC	2999
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OY	3120	CCTGAC	CCG	CACT	TCAC	CACT	TGAG	AG	AG	AC	CG	GC	CA	AA	3179
Db	3228	CTTGGA	TCC	CACT	TCAC	CACT	TGAG	AG	AG	AC	CG	GC	CA	AA	3287
OY	3180	GCAGCGG	AGG	SCA	AG	AG	CTG	TA	GGG	CA	AG	AT	T	T	3239
Db	3288	GCAGCGG	AGG	SCA	AG	AG	CTG	TA	GGG	CA	AG	AT	T	T	3347
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Db	3348	AA													

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QY	3360	ACCAAGGTTGCCGTCGCGCAGACACATGTGGAGTTCTGGGAGAGCGCTTTAAAGGCT	3419
Db	3468	ACCAAGGTTGCCGTTTGGCCAGGACCACTGGAGTTCTGGGAGAGTGTCTTCAAGGCT	3527
QY	3420	CACCCATAGACCCCATTTCTTGTCCAGACTAAGCAGCGAGACAATTCCCTA	3479
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QY	3480	CCTGTAGACACAGGCTACGGTGTGGCGCCAGGGGTGTAAGGTGTCACCTCATGTGGGA	3599
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QY	3540	CCAATGTGGAAGTGTCTCATACGGGTAAAGGCTACGCTACGTCAGCGGCCAACGCCCTGCT	3599
Db	3648	TCAATGTGGAAGTGTCTCATACGGGTGAAGCTACGCTGCGACGGGCCAAACCCCTTGCT	3707
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QY	3660	CATGGCATGATGTCGGCTGACCTGGAAGTGTACAGGACACCTGGTGTGTAGCGCG	3719
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QY	3780	GATCATCTTGTCCGAAAGCGCGGCATCATTCGCGACAGGAGAACTCTTACCGGAGTT	3839
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QY	3840	CGATGAGTGGAGAGTGGCGGCTACACCTCCCTTACATCGAACAAGGATGACACTGCG	3899
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QY	3900	CGAACATTTCAACAGAAAGCATTCGGGTTGCTGCAACAGCGCCACCAAGCGGAGCG	3959
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APPLICANT: OKAYAMA, Hiroto			
APPLICANT: FUKE, Isao			
APPLICANT: MORI, Chisato			
APPLICANT: TAKAMIZAWA, Akahisa			
APPLICANT: YOSHIDA, Iwao			
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC			
NUMBER OF SEQUENCES: 50			
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ADDRESSEE: Armstrong, Westerman, Hattori, Mcleland &			
ADDRESS: Naughton			
STREET: 1725 K St. N.W. Suite 1000			
CITY: Washington			
STATE: D.C.			
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ZIP: 20006			
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COMPUTER: IBM PC compatible			
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ATTORNEY/AGENT INFORMATION:			
NAME: Mcleland, Le-Nhung			
REGISTRATION NUMBER: 31,541			
REFERENCE/DOCKET NUMBER: 900703G			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (202) 659-2930			
TELEFAX: (202) 887-0357			
INFORMATION FOR SEQ ID NO: 31:			
SEQUENCE CHARACTERISTICS:			

LENGTH: 7917 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
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LOCATION: 1..7516
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us-09-315-850-31

Query Match 65.3%; Score 5218; DB 4; Length 7917;
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QY 6240 GGAAGCCTGTAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAA 6299
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QY 6300 GGAGCTCGGAGCTATCCAGCAAGGCCGTTAACCAATCCGCTCCGTTGGAGAGACT 6359
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QY 6360 GCTGGAAGACACTGAGACACCAATTTGACACCACCATCATGGCAAAATAGAGTTTCTG 6419
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Db 6588 AGTCGCTGTATGCGAGAAAGATGGCCCTTATGATGTGCTCCACCCTCCCTAGGCGCT 6647
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QY 6900 GAAGCTCCAGGACTGACAGATGCTGATGCGAGAGACGACCTTGTCTGTAAG 6959
Db 7008 GAAGCTCCAGGACTGACAGATGCTGATGCGAGAGACGACCTGCTGTAAGTGAAG 7067
QY 6960 CGCGGGAGCCCAAGAGGACGAGGGAGCTTACGGCTTACAGAGGCTATGACTAGATA 7019
|||||

Db 7068 CGCGGGAGCCCAAGAGAGACCGGGCGAGCCTACAGTCTTACAGAGGCTATGACTAGATA 7127
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Db 7308 CTCTGCTAGGCAACATTTATATGATGCGCCACTTGTGGCAAGGATGATCTCTGAT 7367
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QY 7800 TTTTCCCTTT 7809
Db 7908 TTTTCTTTT 7917
RESULT 6
US-08-324-977-1
; Sequence 1, Application US/08324977
; Patent No. 5747339
; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
; APPLICANT: MORI, Chisato
; APPLICANT: TAKAMIZAWA, Akahisa
; APPLICANT: YOSHIDA, Iwao
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:

Mon Jun 2 08:44:25 2003

us-10-005-469-4.rn1

Page 18

ADDRESS: Armstrong, Westernman, Hattori, Mcleland &
ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in. 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
FEATURE:
NAME/KEY: CDS
LOCATION: 333..9362
US-08-324-977-1

Query Match	65.3%	Score 5218:	DB 1:	Length 9416:
Best Local Similarity	91.8%	Pred. No. 0:		
Matches 5515:	Conservative	0: Mismatches 495:	Indels 0:	Gaps 0:
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QY 1860	TAGCCTCACAGCGCGGAGACAGAGACAGGTCCAGGGGAGAGTCCAGTGTGTCCACCG	1919		
Db 3467	TAGCCTACAGGCGGGAGACAGACAGGTCCAGGAGAGGTTTCAGGTGGTTCCACCG	3526		
QY 1920	AACGCAATCTTCTCTGGCCAGCACTGGCTCAATAGCGCTGTGTGAGCTMTATATATGTC	1979		
Db 3527	AACGCAATCTTCTCTGGCGACTGGCTCAACGGCGCTGTGTGACCGTTTACATATGTC	3586		
QY 1980	CGGCTCAAGACCCCTTGGCGGCGCCCAAGGCGCCCAATCACCCAAATGTATACCAATGTGA	2039		
Db 3587	TGGCTCAAGAACCTTATAGCCCGCCGCAAGGGGCGCCCAATCACCCAGATGTATACATATGTGA	3646		

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Db	3647	CCAGACCTGCTGGGTGGCAGAGCGCCCCCGGGGGCGGTTCCTTAGACACTGACACTG	3706
QY	2100	CGGACGCTGGACCTTTACTTGGTGCAGAGCAATGCGATGCTATTCGGTGCGCCGGCG	2159
Db	3707	TGGACGCTAGACCTTTACTTGGTGCAGAGCAATGCTATTCGGTGCGCCGGCG	3766
QY	2160	GGGGGACAGAGGGGGAGGCTACTCTCCGCCAGCGCCGTCTCCACTTGAAGAGCTTTC	2219
Db	3767	GGGGGACAGTAAAGGGAGGCTGCTCTCCGCCAGCGCTCTCTACTTGAAGAGCTTTC	3826
QY	2220	GGGGGCTCAGTCTGTGCCCCGTGGGGCAGGCTGTGGGCACTTTTGGGCTGCGCTGTG	2279
Db	3827	GGGGGCTCAGTCTGTGCCCCGTGGGGCAGGCTGTGGGCACTTTTCCGGGCTGGCGATG	3886
QY	2280	CACCCGAGGGGGTGTGCAAGAGCGGTGAGCTTTTACCCCTCAGCTCTAAGAAACACTAT	2339
Db	3887	CACCCGAGGGGGTGTGCAAGAGCGGTGAGCTTTTGTGCCCTTAAGTCCATGAAATACTAT	3946
QY	2400	GGCCCATCTACAGGCCCTACTGTGTAGGGGCAAGAGCACTAAGGTGCGGGTGGATTC	2459
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QY	2460	AGCCCAAGSATAAGGTGCTGTCTGTGAACCCGTCCGTCCGCCACCTTAGTTCGG	2519
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Db	4127	GGCCTATATGTCAAGGACATGTGTTCACACCTCAACATCAAGAACCGGGGTAAAGACAT	4186
QY	2580	CACCCAGGGTCCCCCATCAGTACTCCACCTAATGCAAGTTCTTCTGGCCACGGTGGTG	2639
Db	4187	TACCAAGGGGCCCCGTGCACAACTCTACCTAATGGAAGTTCTTGGCCAGTGGTGGTG	4246
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QY	2760	GCTGCGCACCGCTACGGCTCCGGGATCGGCTCAACCGTGCACATCCCAACATCGAGAGT	2819
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Db	4427	GGCTGTGTCTATGTAAGTAAGTATCCCTTCTATATGGCAAAGCAATCCCATTTGAAGCAT	4486
QY	2880	CAAGGGGGGAGGACACTCATTTTCTGCATTTCCAGAGAANAATGTGATGAGCTGCCGC	2939
Db	4487	CAGGGGGGAGGACACTCATTTTCTGCATTTCCAGAGAANAATGTGATGAGCTGCCGC	4546
QY	2940	GAACTGTCCGGCTCGGACATCAATCTGTAGATATTTCCGGGGGCTTGATGTATCCGT	2999
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QY	3000	CATACCAACTAGCGGAGACGCTCATTTGCTGCATTTCCAGAGCAAGCCTCTTAATGACGGCTTAC	3059
Db	4607	CATACCAACTATCGAGACGCTCTGTTGCTGTGTCATTCAGAGAAGCCTCTGATAGAGCGGTATAC	4666
QY	3060	CGGGATTTGACACTAGTATGCACTGCAATATACATGTGCACCCAGAGAGTGCATTCAG	3119
Db	4667	GGGCACTTTACACTAGTATGCACTGTATACACTATGTGTACCCAGACAGTGTGACTTAG	4726
QY	3120	CCTGAGCCGACCTTACCAATTAGAGAGCAGCAGCTGCCACAAGACGGGTGTACGCTC	3179

Db 4727 CTTGATGCCACCTTACCACTTGAGACGACCGTCCCAAGACGAGTGTGCGCTC 4786
Qy 3180 GCACGGGAGGACGAGCTGATAGGGGACGAGATGGCATTTACAGTTTGTGACTCCAG 3239
Db 4787 GCACGGGAGGATAGGACTGGACGGGTAGGAAAGGCATTTACAGTTTGTGACTCCGG 4846
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Qy 3720 AGCTTAGACCTGTGGCGCGGTATGCTGCTGACAAACAGGAGCGTGTCTTGTGGAGCG 3779
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Qy 3780 GATCATCTTGTCCGGAAGCGCGCATTCCTCCGACAGGGAAGTCTTTACGGGAGTT 3839
Db 5387 GATCATCTTGTCCGGAAGCGCGCATTCCTCCGACAGGGAAGTCTTTACGGGAGTT 5446
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Db 6887 GGTAGGCTAGGCTGGCGGACGAGGATGTCGCCCTCTGAGGACGATCAGACTAGCCA 6946

QY	5340	GCCTCTGGCCCTTCCTCTTAAGGCAACAGCACTACCCGTATGACTCCCGGAGCGCTGA	5399
Db	6947	GTTGTCTGGCCCTTCCTTAAGGCGACATGCACTACCCACATGTCTCTCCGAGCGCTGA	7006
QY	5400	CCTCATCGAGGCCAACCTCCTGTGGGGGAGAGATGGGCGGGAACATCACCCCGGTGA	5459
Db	7007	CCTCATGAGAGCCAACTCCTGTGGGGGAGAGATGGGCGGGAACATCACCCCGGTGA	7066
QY	5460	GTCAGAAATAAGGTGTATTTTGGACCTTTCGAGCGGCTCCAAAGCGAGGAGGATGA	5519
Db	7067	GTCGGAATAAAGGTGTATCTGAGACTCTTTCGACCCGCTTGAGCGAGGAGGATGA	7126
QY	5520	GAGGGAAGTATCCGTTCCGGCGAGATCTCGGAGGATCCAGGAATTCCTCGAGCAT	5579
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Db	7187	GCCCATATGGGCGCCCGGATATPACAACCTCCACTGTATGAGTCTTGAAGACCCGA	7246
QY	5640	CTACGTCCTCCATGATGATACbGgGTGTCCATTCGCGCTCCAGSCCCTCCGATAC	5699
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QY	5880	CTCTCCATCGCCCCCTTGAAGGGAGCCGGGGATCCCATCTCAGCAGGgTCTTG	5939
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Db	7547	GCTTACCTATGACGAGAGGCTATGAGATGTCTGTCTGCTGATGATCCTACATG	7606
QY	6000	GACAGGCGCTGATCACGCGATGCGCTGGGAGGAACCAAGCTGCGCATATACACT	6059
Db	7607	GACAGGCGCTTGTATACGCGCATGCGCTGGGAGGAACCAAGCTGCGCATATACCGCTT	7666
QY	6060	GAGCAACTCTTGTCTCGTGCACGCAACTTGTCTATGCTATACATCTCGAGCGCAG	6119
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QY	6120	CCTGGGAGAAAGATGACACTTGTACATACGACAGTCTGAGACGACACTACCGGA	6179
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QY	6180	CGTGTCTAAGAGATGAAGGGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGA	6239
Db	7787	CGTGTCTAAGAGATGAAGGGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGA	7846
QY	6240	GGAACCTGTAAAGTGAAGCCGCCACATTTGGGCAAGTCTAAATTTGGTATGGGGCAA	6299
Db	7847	GGAACCTGTGAAGTGAAGCCGCCACATTTGGGCAATTCAAATTTGGTATGGGGCAA	7906
QY	6300	GGAGCTCGGAACCTATCCACAGAGCGCGTTAACACATCCGCTCCGTGGAAGACTT	6359
Db	7907	GGAGCTCGGAACCTATCCACAGAGCGCGTTAACACATCCATCCGCTGGAAGACTT	7966
QY	6360	GCTGGAAGACACTGAGACACCAATTGACACCACTATACGCAAAAATGAGgTTTTCTG	6419
Db	7967	GCTGGAAGACACTGTGACACCAATTGACACCACTATATGCAAAAATGAGgTTTTCTG	8026

QY	6420	CGCAACACGAGAGAGAGGGGGGGGGGCGAAGCGACACTGCGCTTAACGATATCCCAATTTGGG	6479
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QY	6540	GATGGCGCTTTTCATAGGAGATTCCAAATACCTCTCTGGACAGAGGGGTCCAGATTCCGTGGAA	6599
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RESULT 7
US-08-384-616-1
; Sequence 1, Application US/08384616
; Patent No. 5847101
; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, HIROTO
; APPLICANT: FUKU, ISAO
; APPLICANT: MORI, CHISATO
; APPLICANT: TAKAMIZAWA, AKAHISA
; APPLICANT: YOSHIDA, IWAO
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Westernman, Hallori, Mcleland &
; STREET: 1725 K St. N.W. Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,616
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/769,996
; FILING DATE: 02-OCT-1991
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-230921
; FILING DATE: 31-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens-Smith, Theresa M.
; REGISTRATION NUMBER: 36,281
; REFERENCE/DOCKET NUMBER: 900703B
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 333..9362
US-08-384-616-1

Query Match 65.3%; Score 5218; DB 2; Length 9416;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;

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RESULT 8
US-08-904-686A-1
Sequence 1, Application US/08904686A
Patent No. 5998130
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKU, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
NUMBER OF INVENTIONS: CDNA AND ANTIGEN POLYPEPTIDE
CORRESPONDENCE ADDRESS: 50

ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., 1.44MB
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mclelland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA from genomic RNA
FEATURE:
NAME/KEY: CDS
LOCATION: 333..9362
US-08-904-686A-1
Query Match 65.3%; Score 5218; DB 2; Length 9416;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;

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Mon Jun 2 08:44:25 2003

us-10-005-469-4.rn1

Page 26

[illegible]

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1      RESULT 9
2      : Sequence 1, Application US/09315850
3      : Patent No. 621872
4      : GENERAL INFORMATION:
5      : APPLICANT: OKAYAMA, Hiroto
6      : APPLICANT: FUKU, Isao
7      : APPLICANT: MORI, Chisato
8      : APPLICANT: TAKAMIZAWA, Akahisa
9      : APPLICANT: YOSHIDA, Isao
10     : TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
11     : TITLE OF INVENTION: CNA AND ANTIGEN POLYPEPTIDE
12     : NUMBER OF SEQUENCES: 50
13     : CORRESPONDENCE ADDRESSES:
14     : ADDRESSEE: Armstrong, Westernman, Hattori, Mcleland &
15     : STREET: 1725 K St. N.W. Suite 1000
16     : CITY: Washington
17     : STATE: D.C.
18     : COUNTRY: U.S.A.
19     : ZIP: 20006
20     : COMPUTER READABLE FORM:
21     : MEDIUM TYPE: Diskette, 3.5 in., 1.44MB
22     : COMPUTER: IBM PC Compatible
23     : OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
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26     : APPLICATION NUMBER: US/09/315,850
27     : FILING DATE:
28     : PRIOR APPLICATION DATA:
29     : APPLICATION NUMBER: US/08/904,686
30     : FILING DATE: 01-AUG-1997
31     : APPLICATION NUMBER: US 08/324,977
32     : FILING DATE: 18-OCT-1994
33     : PRIOR APPLICATION DATA:
34     : APPLICATION NUMBER: JP 2-167466
35     : FILING DATE: 25-JUN-1990
36     : PRIOR APPLICATION DATA:
37     : APPLICATION NUMBER: JP 2-230921
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41     : FILING DATE: 09-NOV-1990
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OY 4140 TACCTCTGTTTAAACATCTGCGGGGATGCGGCGCCCAACTGCTCTCCACAGCG 4199
Db 5747 TACCTCTGTTTAAACATCTTGGGGGATGCGGCGCTGCGCCCAACTGCTCTCCACAGCG 5806
OY 4200 TGCTCTGCTTGTGAGGCGCGGATCGCTGAGGCGGCTGTGGGCGCATAGGCGCTGG 4259
Db 5807 CGCTTCGCGCTTTCGCGGCGCGGATCGCGGCTGTGGGCGCATAGGCGCTGG 5866
OY 4260 GAAGTGCTTGTGATATTTTGGCAGGTATGAGAGCAGGGGTGAGCAGCGCTCGTGGC 4319
Db 5867 GAAGTGCTTGTGATATTTGCGGGGTATGAGAGCAGGAGTGGCGCGCGCTCGTGGC 5926
OY 4320 CTTTAAAGTCAAGAGCGGCGAGATGCCCTCCAGCAGGAGACTGGCTACTACTCCCTGC 4379
Db 5927 CTTTAAAGTCAAGAGCGGCGAGATGCCCTCCAGCAGGAGACTGGCTACTACTCTCTGC 5986
OY 4380 TATCTCTCCCTGCGCGCCCTAGTGTGCGGGGTGCTGCGCAGCGATCTGCTGCGCA 4439
Db 5987 CATCTCTCTCTGCGCGCCCTGCTGTGCGGGGTGTGTGTCAGCAATACTGCTGCTGCA 6046
OY 4440 CGTGGGCCAAGGAGGGGGGTGTGCAATGAGTAACCGGCTGATACCGTTCCTCGCGC 4499
Db 6047 CGTGGGTTCGGGAGAGGGGGGTGTGCAATGAGTAACCGGCTGATACCGTTCCTCGCGC 6106
OY 4500 GGGTAAACAGTCTCCCGCAGCAGCTATGTGCTGAGAGGAGAGGCTCAGACAGCTGAC 4559
Db 6107 GGGTAAATCATGTTTCCCGCAGCACTATGTGCTGAGAGGAGAGCGCGCTGCTGAC 6166
OY 4560 TTAGATCTCTCTAGTCTTACCATCACTCAAGTCTGTAAGAGGCTTACCAAGTGAATCA 4619
Db 6167 TTAGATCTCTCTAGTCTTACCATCACTCAAGTCTGTAAGAGGCTTACCAAGTGAATCA 6226
OY 4620 CGAGACTGCTCAAGCGCATCTCGGCTCGTGGCTAAGAGATGTTGGATGGATAG 4679
Db 6227 TGAACACTGCTCAACACCGCTGTTCGGGCTCGTGGCTAAGGATGTTGGGACCTGAGTATG 6286

OY 4680 CACGCTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGATGCCCGG 4739
Db 6287 CACGCTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGATGCCCGG 6346
OY 4740 AGTCCCTTCTTCATGATCACTGAGGCTCAAGAGGATGTGGCGGGGACAGGCAATCA 4799
Db 6347 AGTCCCTTCTTCATGATCACTGAGGCTCAAGAGGATGTGGCGGGGACAGGCAATCA 6406
OY 4800 GCAACCACTGCGCATGTGAGGACAGACATCACCGCATGTGAAAAAGGTTCCATGAG 4859
Db 6407 GCAACCACTGCGCATGTGAGGACAGACATCACCGCATGTGAAAAAGGTTCCATGAG 6466
OY 4860 GATCTGGGGGCTAGACCTGTAGTACAGCTGGCATGGAACATTCCTCCATTAACCGTA 4919
Db 6467 GATCTGGGGGCTAGACCTGTAGTACAGCTGGCATGGAACATTCCTCCATTAACCGTA 6526
OY 4920 CACCAAGGGCCCTGCAAGCCCTCCCGGCGCAATTTATTTAGGGCGCTGTGGCGGT 4979
Db 6527 CACCAAGGGCCCTGCAAGCCCTCCCGGCGCAATTTATTTAGGGCGCTGTGGCGGT 6586
OY 4980 GCGTCTAGSAGATACGTGGAGGTTACGGCGGTGGGGATTTCCACTACTGACGGGCA 5039
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OY 5040 GACCACTGACAAAGTAAAGTCCCGTGTGAGGTTCCCGGCCCGAAATTTCTTCAAGAGT 5099
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OY 5100 GGAATGGGTGGCGTTGCAAGAGTACGCTCCAGCGTGCAGAACCCCTCTACGAGAGAGT 5159
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OY 5160 CACATTCCTGCTGGGCTCAATCAATACCTGTTGGGTGCTACAGCTCCCATGAGAGCGCA 5219
Db 6767 TACATTCAGGTCGGGCTCAACCAATACCTGTTGGGTGCTACAGCTCCCATGAGAGCGCA 6826
OY 5220 ACCGAGCTAGCAGTGTCTCACTTCCATGCTCACCGACCCCTCCCACTTACGGGAGAG 5279
Db 6827 ACCGAGTGTACAGTGTCTCACTTCCATGCTCACCGACCCCTCCCACTTACGGGAGAG 6886
OY 5280 GAGTAAAGGATAGGCTGGGCGAAGGATCTCCCGCTCTTGGAGAGCTCATCACTGAGCA 5339
Db 6887 GAGTAAAGGATAGGCTGGGCGAAGGATCTCCCGCTCTTGGAGAGCTCATCACTGAGCA 6396
OY 5340 GCTGTCTGCGCTTCTTGAAGGCAACATGCACTACCGGTATGACTCCCGGAGCGTGA 5399
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OY 5400 CCTCATGAGGCAACCTCCGTGGGGGCAAGAGATGGGGGGAACATCCCGCGGTGA 5459
Db 7007 CCTCATGAGGCAACCTCCGTGGGGGCAAGAGATGGGGGGAACATCCCGCGGTGA 7066
OY 5460 GTCAAGAAATAGGTAGTAAATTTTGAAGTCTTTGAGCGCTCCAAAGGAGAGATGA 5519
Db 7067 GTCAAGAAATAGGTAGTAAATTTTGAAGTCTTTGAGCGCTCCAAAGGAGAGATGA 7126
OY 5520 GAGGGAAGTATCCGTTCCGGGGGAGATCTGCGGAGGTTCAGGAAATCTCCTCGAGGAT 5579
Db 7127 GAGGGAAGTATCCGTTCCGGGGGAGATCTGCGGAAATTCAGGAAATCTCCTCGAGGAT 7186
OY 5580 GCCCATATGAGGACGCCCGGATTAACAACCTTCATCTTGAAGTCTGGAAGAGACCCGA 5639
Db 7187 GCCCATATGAGGACGCCCGGATTAACAACCTTCATCTTGAAGTCTGGAAGAGACCCGA 7246
OY 5640 CTACGTCCCTCGAGTGAAGCAGGGGTGTCATTGTCCTCCCGCAAGGCGCCCTCGATAC 5699
Db 7247 CTACGTCCCTCGAGTGAAGCAGGGGTGTCATTGTCCTCCCGCAAGGCGCCCTCGATAC 7306
OY 5700 ACCCTCAGGAGAGAGAGAGAGGTTGTCTGTCAAGTATCAACGATGCTCTCTGCTGAG 5759
Db 7307 ACCCTCAGGAGAGAGAGAGAGGTTGTCTGTCAAGTATCAACGATGCTCTCTGCTGAG 7366

QY	5760	GGAGCTCGCCAAACCAACCTTGGGAGCTCCGACATCTGTCGCCCGTCGACACGGCCAGGC	5819
Db	7367	GGAGCTCGCTACTAAACACTTGGGAGCTCCGAAATCATTCGGCCGTCGACACGGCCAGGC	7426
QY	5820	AACGGCTCTCTCGACCCACCCCTCCGAGCAGCGCCACCGGGATCCACGTTGAGTGTGA	5879
Db	7427	GACCGCCCTTCTCGACCAAGGCTCCGACACCGGTGACAAAGATCCGACGTTGAGTGTGA	7486
QY	5880	CTCTCCATGCCCCCTTGGAGGGAGCGCGGGGATCCCGATCTCACGACGGGTCTTG	5939
Db	7487	CTCTCCATGCCCCCTTGAAGGGGGAACCGGGGACCCCGATCTCACTGACGGGTCTTG	7546
QY	5540	CTCTACCGTAAAGCAGAGAGGCTAAGTGAAGACTCTCTGTGTCTCGATGTCTTACATAG	5999
Db	7547	GTCCTACCGTAGAGGAAGAGCTAAGTGAAGATCTCTGTGTCTCTCAATGTCTTACACTG	7606
QY	6000	GACAGCGCCCTGATCAGCGCATGCGCTCGGAGGAAACCAAGCTGCCATCAATGCACT	6059
Db	7607	GACAGCGCCCTTATGATCAGCGCATGCGCTCGGAGGAAAGCAAGCTGCCATCAAGCATT	7666
QY	6060	GAGCAATCTTTTCTCTCCGTCACACACACTTGGTCTAATGCTAACAATCTCCAGCGCAAG	6119
Db	7667	GAGCAATCTTTTCTCTGCGCACCATTACATGGTTATGTCACAAATATCTCCAGCGCGG	7726
QY	6120	CTTCGCGCAGAAAGGTCACCTTTTGACAGACTGCAAGTCTCTGACGACACACTACCGGA	6179
Db	7727	CTTCGCGCAGAAAGAGTCACTTTTGACAGACTGCAAGTCTCTGACGACACACTACCGGGA	7786
QY	6180	CGTGCTCAAGAGATGAAGCGCAAGCGCTCCACAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA	6239
Db	7787	CGTGCTCAAGAGATGAAGCGCAAGCGCTCCACAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA	7846
QY	6240	GGAAGCTGTAGCTAGCGCCCCACACTTTCGGCCACATCTAAATTTGGCTATGGGGCAA	6299
Db	7847	GGAAGCTGTAGACTGAGCGCCCCACACTTTCGGCCAAATCAAGTTTGGCTATGGGGCAA	7906
QY	6300	GGAGCTCGGAACTTTCACGCAAGGCGGTTAACCAATCGGCTCCGCTGGGAAGCACT	6359
Db	7907	GGAGCTCGGAACTTATCCAGCAAGGCGGTTAACCAATCGGCTCCGCTGGGAAGCACTT	7966
QY	6360	GCTGGAAGACACTGAGACACCAATTGACACACCAATCATGCGCAAAAAAATGAGTTTCTG	6419
Db	7967	GCTGGAAGACACTGTGACACCAATTGACACACCAATCATGCGCAAAAAAATGAGTTTCTG	8026
QY	6420	CGTCCACACGAGAAGGGGGGCGCGCAAGCAGTGGCTTATGATTCGATCCAGATTGGG	6479
Db	8027	TGTCACACCGAGAAAGGAGGCGGTAAAGCAGCGCCCTTATGATTCGATCCAGATCTGGG	8086
QY	6480	GTTTGTGTGTGCGAGAAAAATGGCCCTTTAGATGTGTCTCCACCTCTCCCAAGCCGT	6539
Db	8087	AGTCCGTGTGTGCGAGAAAGATGGCCCTTATGATGTGTCTCCACCTCTCCCAAGCTGT	8146
QY	6540	GATGGGCTCTTATAGGATTCGAATACACTCTCTGGACAGGGGCGAGTTCTCTGTGAA	6599
Db	8147	GATGGGCTCTCTATAGGATTCGAATACACTCTCTGGGACAGGATTCGATTCCTGTGAA	8206
QY	6600	TGCTGGAAGACGAAGAAATGCCCTATGGGCTTCGATATGACACCCGCTGTTTGACTC	6659
Db	8207	TACCTGGAATATCAAGAAAAACCCCATGGGCTTTCTATGTGACACTCGCTGTTTGACTC	8266
QY	6660	AAGGCTACAGAGATACACTCCGTGTGAGAGGTCAATCTCCATGTCATGTGTGACTTGGC	6719
Db	8267	AAGGCTACCCGAGACGACACTCCGTGTGAGAGGTCAATTTACCATGTGTGTGACTTGGC	8326
QY	6720	CCCCGAAAGCAGACAGSCCATTAAGTGCTCACAGAGCGGCTTTACATGGGGCCCTCT	6779
Db	8327	CCCCGAAAGCAGAGAGCCCATTAAGTGCTCACAGAGCGGCTTTATGCGGGGCTCTCT	8386
QY	6780	GACTAATTTTAAAGGGGAGAACTGCGGCTTTCGCGGTTCGCGGCGAGGCGGTACTAC	6839
Db	8387	GACTAATTTTAAAGGGGAGAACTGCGGTTATGCGCGGTTCGCGGCGAGGCGGTCTGAC	8446
QY	6840	GACCAAGCTCGCGTAAATACCTCACATGTTACTTGAAGGCCCTCGCGGCTGTGACAGTCC	6899

[illegible]

RESULT 10
US-08-823-895A-27
; Sequence 27, Application US/08823895A
; Patent No. 6433159
; GENERAL INFORMATION:

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APPLICANT: Kevin P. Anderson
 TITLE OF INVENTION: Compositions And Methods For
 TITLE OF INVENTION: Treatment Of Hepatitis C Virus Associated Diseases
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jane Massey Licata, Esq.
 STREET: 66 E. Main Street
 CITY: Marlton
 STATE: NJ
 COUNTRY: USA
 ZIP: 08053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 COMPUTER: IBM 486
 OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/823, 895A
 FILING DATE: March 17, 1997
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/453, 085
 FILING DATE: May 30, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/945, 289
 FILING DATE: September 10, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane Massey Licata
 REGISTRATION NUMBER: 32,257
 REFERENCE/DOCKET NUMBER: ISPH-0203
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (609) 779-2400
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 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9416
 TYPE: Nucleic
 STRANDEDNESS: Single
 TOPOLOGY: linear
 ANTI-SENSE: NO
 OS-08-823-895A-27

Query Match	65.3%	Score 5218:	DB 4:	Length 9416:
Best Local Similarity	91.8%	Pred. No. 0:		
Matches 5515:	Conservative	0:	Mismatches 495:	Indels 0:
			Gaps	0:
QY 1800	CATGGCCCTATTATCGGCTACTGCCACAGACGGAGGCCCTACTTGGCTGCATCATCAC	1859		
Db 3407	CTTGCGGCCCATCACGGCTACTTCCCAACAGACGGGGGCTACTTGGTGCATCATCAC	3466		
QY 1860	TACGCTCACAGGCGCGGGAAGAGAACACAGGTGAGGGGAGGTCACAGTGGTTCACACCG	1919		
Db 3467	TAGCTTTACAGGCGCGGGAAGAACACAGGTGAGGGAAGGTATAGGTGGTTCCACCG	3526		
QY 1920	AACACATCTTTTCTGCGCACCTGGCTCAATGGCTGTGTGGAGCTCTATCATGGTGC	1979		
Db 3527	AACACATCTTCTCTGGCACCTGGCTCAAGGGCGTGTGTGGACGTTTACCATGGTGC	3586		
QY 1980	CGGCTCAAGAACCCCTTGCCGGGCCAAGAGGGCCCAATCCCAATATGACACCAATGTGA	2039		
Db 3587	TGGCTCAAAACCTTATGGCGGCCCAAGGGGGCCATCACCCAGATGTACACTATATGTGA	3646		
QY 2040	CCAGGACCTGTGGGTGGCAAGGCGCCCCCGGGGCGGTTCCCTGACACCATGCACTG	2099		
Db 3647	CCAGGACCTGTGGGTGGCCAAAGCCCCCGGGGCGGTTCTTGGACCATGCACTG	3706		
QY 2100	CGGACGCTCGACACTTACTTGGTACAGAGAGCATCCGATGTCAATTCGGGTGGCGGGCG	2159		
Db 3707	TGGACGCTCAGACCTTACTTGGTACAGAGACATCTGACGTCAATTCGGGTGGCGGGCG	3766		
QY 2160	GGGCGACAGCAGGGGGAGGCTACTCTCCCCACAGGCGCGTCTTCTCACTTGAAGGGCTTTC	2219		
Db 3767	GGGCGACAGTGAAGGGAGGCTGCTCTCCCCACAGGCGCGTCTTCTCACTTGAAGGGCTTTC	3826		

QY	2220	GGGGGTCACACTGCTGCCCCCGGGGGAGACGCTGTGGGCAATCTTGCGGGCTCGCTGTG	227
Db	3827	GGG1GGTCCACTGCTGTGCCCCCTTGGGGACAGCTGTGGGCAATCTTGCGGGCTCGCTGTG	3886
QY	2280	CACCCGAGGGGTTGGCGAAGCGGTGGACCTTTGTACCGTGCAGTCTATGGAAACACTAT	2339
Db	3887	CACCCGGGGGTTGGCGAAGCGGTGGACCTTTGTACCGTGCAGTCTATGGAAACACTAT	3946
QY	2340	GGGCTCCCGGCTCTACGAGCAACCTGTCGCCCTCCGGCGGTACCGGCAATTCGAGT	2349
Db	3947	GGGCTCTCCGGCTCTTCCAGGCAACTGTAATCCGCCCGGCGGTACCGGCAATTCGAGT	4006
QY	2400	GGCCCATCTACAGCGCCCTTACTGTAGCGGCGCAAGACACTAAGTGGCGGCTGGATGC	2459
Db	4007	GGCCCATCTACAGCTCTCCACTGTGACGCGGCAAGATACTAAGTGGCGGCTGGATATGC	4066
QY	2460	AGCCCAAGGGATTAAGGTGGTTGGTTCGTGAACCGGTCCGGCGGCAACCTAGTTTG	2519
Db	4067	AGCCCAAGGGATTAAGGTGGTTGGTTCGTGAACCGGTCCGGCGGCAACCTAGTTTG	4126
QY	2520	GGCGTATATGTTTAAGGCACATGGTATCGACCTTAACATCAGAACCGG99TAAGACCAT	2579
Db	4127	GGCGTATATGTTTAAGGCACACAGGTATTTGCCACCAATCAGAACCTGG99TAAGACCAT	4186
QY	2580	CACACAGGGTGGCCCCCATACAGTACGTCCACACTATGGGCAAGTTTCTTGGCGAGGTGGT	2639
Db	4187	TATCACAGGCGCCCCCTTCATACTCTACTTATGGCAAGTTTCTTGGCGAGGTGGT	4246
QY	2640	CTCTGGGGGGCCCTATGACATTCATTAATATGTATGATGTGCCACTGACCTGACTGCACAC	2699
Db	4247	CTCTGGGGGGCCCTTATGACATTCATTAATATGTATGATGTGCCACTGACCTGACTGCATAC	4306
QY	2700	TATCCTGGGCAATGGGGACACATTCCTGGAGCGCAAGCGGAGAGCGGTGGGCGGCACTGTGT	2759
Db	4307	AATCTTGGGCAATGGGGACACATTCCTGGAGCGCAAGCGGAGAGCGGTGGGCGGCACTGTGT	4366
QY	2760	GCTGCGCACCGCTACGCCCTCCGGGATTCGTACCGGTGCCACATCCAAACATCGAGGAGT	2819
Db	4367	GCTGCGCACCGCTACGCCCTCCGGGATTCGTACCGGTGCCACACCCAAACATCGAGGAGT	4426
QY	2820	GGCTGTGGCCAGCTGAGGAAATTCGCCCTTTTGGCAAGCATCCCATCGAAGCAT	2879
Db	4427	GGCCCTGTCTAATCTGAGAGATTCGCCCTTCTATGGCAAGCATCCCATCGAAGCAT	4486
QY	2880	CAAGGGGGGAGGSCACTTCATTTTCTGCCATTCGAAGAAATGTATGACTGGCGC	2936
Db	4487	CAGGGGGGAGGAGCATCTCATTTTCTGTCAATCCAAAGAAAGTGGAGACTGGCGC	4548
QY	2940	GAACTGTTCGGGCTCGGACATAGTGTAGATATTACGGGGCTTGATGTATTCGT	2999
Db	4547	AAAGTGTCAAGGCTCGGAAATCAAGGTGTGGGTATTACGGGGGCTGTGATGTGCGGT	4606
QY	3000	CATACCACTAGCGGAGACGTCAATGTTCGTAGCAACGAGCGCTCTATATGACGGGCTTAC	3055
Db	4607	CATACCACTATTCGGAACAGCTGTTCGTGGCAACAGCGCTGTATATGACGGGCTATAC	4666
QY	3060	CGGCAATTCACATCAGTATGCAGCTCAATATCATGTGTACACCACAGCATGTGACTTCAG	3119
Db	4667	GGGCGACTTTCATCTCAGTATGCAGCTGTATACATCATGTGTACACCACAGCATGTGACTTCAG	4722
QY	3120	CTGTGACCCGACTTCACATTTAGAGACAGACCGTGGCCACAAGAGCGGTCTCAAGCTC	3177
Db	4727	CTTGTATCCCACTTCACCATTTAGAGAGACCGTGGCTTCAAGAGCAAGTGTGGGCTC	4786
QY	3180	GCAGGCGGAGCGAGCATGTGTAGGGGCGAGATGGGCAATTTACAGGTTTGTACTCCAG	3233
Db	4787	GCAGGCGGCGGATGTAGCATGTGTAGGGGCGAGATGGGCAATTTACAGGTTTGTACTCCAG	4844
QY	3240	AGAAAGGCGCTCGGGCAATGTTCAATTCCTGGTGTCTGTGGAGTGTATAGACGGGGGTG	3299
Db	4847	AGAAAGGCGCTCGGGCAATGTTCAATTCCTGGTGTCTGTGGAGTGTATAGACGGGGGTG	4906

QY	3300	TGTTGGTACGAGCTCAGCCCGCGGAGACGTCAGTTAGTTGGGGCTTACCTAAACAC	3359
Db	4907	TGCTGGTACGAGCTCAGCCCGCGGAGACCTCGGTTAGTTGGGGCTTACCTGAACAC	4966
QY	3360	ACCAAGGTTGCCGCTGTGCCAGAGCAATCTGGAGTTCTGGAGAGCGCTCTTTACAGGCTT	3419
Db	4967	ACCAAGGTTGCCGCTGTGCCAGAGCACTTGAGATTCTGGAGAGTGCTCTTCCACAGGCTT	5026
QY	3420	CACCCACATAGAGGCCCATTTCTTCCACAGCTAAGAGGCGAGAGACACACTCCGCTA	3479
Db	5027	CACCCATATAGATGACACTCTTTCTGTCCACAGCCAGAGGCGAGAGACACTTCCCTTA	5086
QY	3480	CCTGTAGCATACCAAGGCTACGCTGTGGCCAGGGCTCAGGCTCCACCTCCATCTGTGGGA	3539
Db	5087	CCTGTAGCATACCAAGCCACGAGTGTGGCCAGGGCTCAGGCCCCACCTCCATCATGTGGGA	5146
QY	3540	CCAAATGTGGAATGTCTCATAGGCTAAAGCCTACGCTGTGACGGGCGCAACGGCCCGCT	3599
Db	5147	TCAAATGTGGAATGTCTCATAGGCTGAAACTACGCTGCAGGGGCCAACACCTTGTCT	5206
QY	3600	GTAATAGGCTTGGAGCCGTTCAAAACGAGGTACTACACACACCCCATTAACCAATATCAT	3659
Db	5207	GTAACGCTTGGAGCCGCTCAGATATAGAGTCACTCCCTCACCCACCCCATTAACCAATATCAT	5266
QY	3660	CATCGCATGTGATGTGCGCTACCTGGAGGTCGTACAGACACTGGGGCTGTGATAGGCGG	3719
Db	5267	CATGCGATGTGATGTGCGCTACCTGGAGGTCGTACTAGCACCTGGGGCTGTGATAGGCGG	5326
QY	3720	AGTCTTAGCAGCTCTGGCCGCGTATTGCTGTACAACAGGCAAGCTGTGATTTGTGGCAG	3779
Db	5327	AGTCTTTCAGCTCTGTGCCCGCGTATTGCTGTACAACAGGCAAGCTGTGATTTGTGGTAG	5386
QY	3780	GATCATTTTTCGCGAAGGCGCGGCATCATTTCCGACAGGAGAGTCCCTTTACCCGGAGTT	3839
Db	5387	GATTATCTTGTGCGGAGGCGCGGCATTTGTCGCGACAGGAGGTTCTCTACAGAGATT	5446
QY	3840	CGATGAGATGGAAGAGTGGCGCTCACACCTCCCTTATCATCGAACAGGAAATGACAGCTGC	3899
Db	5447	CGATGAATGGAAGAGTGGCGCTTCGCACTCCCTTATCATCGAGCGGAAATGACAGCTGC	5506
QY	3900	CGAACATTCCTAAACAGAGAGGCAATGTGGGTGTGCAACAGCACCAAGCAAGCGAGAGC	3959
Db	5507	CGAGCAATTCAGGACAGAAACGCTCGGGTTACTGTCAACAGCCACCAACCAAGCGAGAGC	5566
QY	3960	TGCTGCTCCCGTGTGGAATCCAAATGTGGGGAGACCCCGAAGCGCTCTGTGGGAGAGCAT	4019
Db	5567	TGCTGCTCCCGTGTGGAATCCAAATGTGGGGAGAGCCCTTGGAGATTTCTGGGAGAGCAT	5626
QY	4020	GTTGAAATTCATACGCGGGATACAAATATTAGAGGCTGTGCTCACTCTGCTGGCAACC	4079
Db	5627	GTTGAAATTCATACGCGGGATACAGTACTTAGAGGCTTATCACTCTGCTGGGAACCC	5686
QY	4080	CGCGATAGCATCATGATGTGCATTCACAGCGCTATACACAGCCCGCTCACACCCACA	4139
Db	5687	CGCATATACCATTTGATGTGCATTCACAGCGCTTATACACAGCCCGCTCACACCCACA	5746
QY	4140	TACCTCTCTGTTTAAACATCCTGTGGGGGATGTGTGGCCGCCCAACTGTGCTTCCAGGC	4199
Db	5747	TACCTCTCTGTTTAAACATCTTGGGGGGGTGTGTGGCCGCCCAACTGTGCTTCCAGGC	5806
QY	4200	TGCTTCTGCTTCTGTAGGCGCGCGGCATCGGTGAGGCGGTGTGGAGCATATAGGCTTGG	4259
Db	5807	CGCTTCTGCTTCTGTAGGCGCGCGGCATCGCGGTGGCGCTGTGGGACATATAGGCTTGG	5866
QY	4260	GAAAGTCTTGTGATATATTTTGGCAGTTATGAGCAGGGGTTGGCAGCGCGCTGTGGC	4319
Db	5867	GAAAGTCTTGTGATATATTTTGGCAGTTATGAGCAGGAGTGTGGCGCGCGCTGTGGC	5926
QY	4320	CTTTAAGGTCATGAGCGGCGAGATGTCCCTCACCGAGACCTGGCTTAACTTACTCCGCG	4379
Db	5927	CTTTAAGGTCATGAGCGGCGAGATGTCCCTCACCGAGACCTGTGTCATTACTTCTCCGCG	5986
QY	4380	TATCTCTTCCCTTGCGGCGCTAGTCTGTGGGGTGTGTGTGCGACAGCATCTGCTGTGGCA	4439

Db	5987	CATCCTCTCTCTGAGCGCCCTGGTCCGTCGTCGGGGGTCGTGTGTGGAGCAATACGTCCCTGACA	6046
OY	4440	CGTGGCCCAAGGGGAGGGGGGCGTGTGCACTGGAGTGAACCGGGCTGATAGGTTCCGTTGGC	4499
Db	6047	CGTGGGTCGGGAGAGGGGCGCTGTGCGAGTGGATGAACCGGCTGATAGGTTCCGTTGGC	6106
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OY	4560	TCGAGTCCTCTCTACTCTTACCATCACTCACTCAAGTGGCTGAAGAGGCTTCAACGATGATCAA	4619
Db	6107	GGGTATTCATGTTTCCCCACGACACTATGTGCTTGAGAGCGACGACGCGGACGCGTGTAC	6166
Db	6167	TCGAGTCCTCTCAAGCTTACCTACCTCACTCACTCTGAAAAGGCTCCACAGTGGATTAA	6226
OY	4620	CGAGGACCTGCTCCACGCCATGCTCCGGGCTCGTGCTAAGAGATGTTTGGGATTGGATATG	4679
Db	6227	TGAAGACTGCTCCACACCGGTGCTCCGGCTCGTGCTAAGGAGATGTTTGGAGCTGGATATG	6286
OY	4680	CAGGGTGTGACGTGAATTCACAGACTGGCTCAAGTCCACGTCACGTCGCCGCAATTGCCGG	4739
Db	6287	CAGGGTGTGACTGACTTCACAGACTGGCTCAAGTCCACGTCGCCGCAACTGCGG	6346
OY	4740	AGTCCCTTCTTCTCATGTCAACGTGGGTACAGAGAGTGTGGCGGGGCGACGCAATCAT	4799
Db	6347	AGTCCCTTCTTCTCGTCGCAACGGGGGTACAAAGGAGTGTGGCGGGGAGCGGCACTCAT	6406
OY	4800	GCAACACACTGGCCATGTGGAGCAACATACCGGACATGTGAATAAAGATTCCATGAG	4859
Db	6407	GCAACACACTGCGCCATGTGGAGCAAGATCACGGGACATGTCAAAAGGTTCCATGAG	6466
OY	4860	GATCGTGGGGCTAGAGACCTGTAGTACAGCTGGCATGGAACATTCCCATTAACGCTA	4919
Db	6467	GATCGTGGGGCTTAAGACCTGTAGCAACATGACATGGAACATTTCCCATTAACGCTA	6526
OY	4920	CACACAGGGGCCCTTGACGCCCTCCCGGGCCCAATATTATTCAGGGGCTGTGGCGGT	4979
Db	6527	CACACAGGGGCCCTTGACGCCCTCTCCAGGCCCAATATTATTCAGGGGCTGTGGCGGT	6586
OY	4980	GGCTGCTGAGGACTACGTGGAAGTTACGCGGGTGGGGGATTTCCCATACGTAGCGGGAT	5039
Db	6587	GGCGCTGAGGAATACGTGGAAGTACGCGGGTGGGGGATTTCCCATACGTAGCGGGAT	6646
OY	5040	GACCACAGAACAGTAAAGTGCCTGTCAAGTTCCCGGCCCGGAATTTCTTACAGAAAGT	5099
Db	6647	GACCACAGAACAGTAAAGTGCCTGTCAAGTTCCCGGCTCTGAAATTTCTTCCGAGAGT	6706
OY	5100	GGATGGGGTCCGTTACACAGTACGCTTCACAGCTGCAAAACCCCTCTACGGGAGAGAGT	5159
Db	6707	GGAGCGAGTCCGTTACACAGTACGCTTCGCGGCTGTGAGGCTCTCTTACGGGAGAGAGT	6766
OY	5160	CACATTCCTGTGTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCATGCGAGCCGA	5219
Db	6767	TACATTCCTGAGTGGGCTCAACCAATACCTGTTGGGTCAAGCTCAACATGCGAGCCGA	6826
OY	5220	ACCGGACGTAGAGTGTCTACTTCCATCTCAACGACCCCTCCCAATTAAGCGGAGAGC	5279
Db	6827	ACCGGATGTAGAGTGTCTACTTCCATCTCAACGACCCCTCCCAATTCACAGCAGAAAC	6886
OY	5280	GGCTAACCTGAGCTGGCCAGGAGGATCTCCGCCCTCTTGCCAGGCTACAGTACCA	5339
Db	6887	GGCTAAGGTAGGTGGCCAGGAGGATCTCCGCCCTCTTGCCAGGCTTACAGTACCA	6946
OY	5340	GCTGTGCGGCTTCTCTTAAGGCAAAATGACACATACCGTATGACCCCGGAGCGCTGA	5399
Db	6947	GTTGTCTGCGCTTCTCTTAAGGCGACATGACATCCACCATGTCTCTCGGAGCGCTGA	7006
OY	5400	CCTCATGAGAGCCAACTCTGTGGCGGAGAGATGGGCGGGGAAATCACCCCGGTGA	5459
Db	7007	CCTCATGAGAGCCAACTCTGTGGCGGAGAGATGGGCGGGGAAATCACCCCGGTGA	7066
OY	5460	GTCGAAAATAGGTATATTTTGGACACTTTCGAGCGGCTCCAGCGGAGAGGATGA	5519

Db 7067 GTGGAGAACAAAGTGTAGTCTGTGACTTTTGGACCCGCTTTCGACGGAGAGAGATGA 7126
QY 5520 GAGGGAATATCCGTTCCGGGGGAGATTCCTGGGAGAGTCCAGGAAATTCCTCGACGAT 5579
Db 7127 GAGGGAATATCCGTTCCGGGGGAGATTCCTGGGAAATCCAGAAAGTTCCCGACGAT 7186
QY 5580 GCCCATATGAGCAGCCCGGATTAACAACCTCCACTGTAGAGTCTGGAAGAACCCGA 5639
Db 7187 GCCCATATGAGGCGCGCGGATTAACAACCTCCACTGTAGAGTCTGGAAGAACCCGA 7246
QY 5640 CTAGTCCCTCCAGTGTACAGCGGTTCCATTGCCGCTGCAAGGCCCTCCGATAC 5699
Db 7247 CTAGTCCCTCCAGTGTGTACAGCGGTTCCACTTCCACTATCAAGGCCCTCCATAC 7306
QY 5700 ACTTCAGAGAGAGAGAGAGAGGTTGTCGTACAAATCTACCGTGTCTTCTGCTGAGC 5759
Db 7307 ACTTCAGAGAGAGAGAGAGAGGTTGTTCTTACAGAGTCCCTGCTTCTGCTTACG 7366
QY 5760 GAGGCTCCGACAAAGACCTTCGAGCTCCGAATCGTCGAGCTGACAGCGAGCGC 5819
Db 7367 GAGGCTCCGCTACTAGAGCTTCGAGCTCCGAATCAATCGGCTGACAGCGAGCGC 7426
QY 5820 AACGGCTCTCTCTGACAGCCCTCGAGAGAGCGGAGCGGAGTCCGACGTTGAGTGA 5879
Db 7427 GACCGCTCTCTCTGACAGCGCTCCGAGAGAGGTGACAAAGATCCAGCTTGAGTGA 7486
QY 5880 CTCTCTCATGCCCCCTTGAGGGGGAGCCGGGGATCCGATCTGACGAGCGGCTTG 5939
Db 7487 CTCTCTCATGCCCCCTTGAGGGGGAGCCGGGGAGCCCGATCTGAGTACGGGCTTG 7546
QY 5940 GCTCTACGCTAAGCGAGAGGCTAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTA 5999
Db 7547 GCTCTACGCTAAGCGAGAGGCTAGTGAAGTGTGCTGCTGCTGCTGCTGCTA 7606
QY 6000 GACAGGCGGCTGATCAGCGCATGCGCTGCGGAGAAACCAAGCTGCCATCATAGCAT 6059
Db 7607 GACAGGCGGCTGATCAGCGCATGCGCTGCGGAGAAACCAAGCTGCCATCATAGCAT 7666
QY 6060 GAGCAATCTTTGCTCCGCTCAGCACTTGTCTATGCTCAACATCTGCGACCGAAG 6119
Db 7667 GAGCAATCTTTGCTCCGCTCAGCACTTGTATGCTCAACATCTGCGACCGAAG 7126
QY 6120 CCTGGGCGAGAGAGTACCTTTGACAGACTGCAAGTCTGAGCAGCACTACCGGA 6179
Db 7127 CCTGGGCGAGAGAGTACCTTTGACAGACTGCAAGTCTGAGCAGCACTACCGGA 7186
QY 6180 CCGTCTCAAGAGATGAAGGGCAGAGGCTCCACAGTAAAGCTTCTATCCGTGA 6239
Db 7187 CCGTCTCAAGAGATGAAGGGCAGAGGCTCCACAGTAAAGCTTCTATCCGTGA 7246
QY 6240 GGAAGCTGTAGCTGAGCAGCCGCTCAATTCGCGCAGATCTAAATTTGGCTAGGGGAAA 6299
Db 7247 GGAAGCTGTAGCTGAGCAGCCGCTCAATTCGCGCAGATCTAAAGCTTCTAGGGGAAA 7306
QY 6300 GGAAGCTGTAGCTGAGCAGCCGCTCAATTCGCGCAGATCTAAATTTGGCTAGGGGAAA 6359
Db 7307 GGAAGCTGTAGCTGAGCAGCCGCTCAATTCGCGCAGATCTAAAGCTTCTAGGGGAAA 7366
QY 6360 GGTGGAAGACTGTGACAGCAATTCAGACCCATCTATGCAAAAATGAGTTTCTG 6419
Db 7367 GGTGGAAGACTGTGACAGCAATTCAGACCCATCTATGCAAAAATGAGTTTCTG 8026
QY 6420 GGTGGAAGACTGTGACAGCAATTCAGACCCATCTATGCAAAAATGAGTTTCTG 6479
Db 8027 GGTGGAAGACTGTGACAGCAATTCAGACCCATCTATGCAAAAATGAGTTTCTG 8086
QY 6480 GGTGGAAGACTGTGACAGCAATTCAGACCCATCTATGCAAAAATGAGTTTCTG 6539
Db 8087 GGTGGAAGACTGTGACAGCAATTCAGACCCATCTATGCAAAAATGAGTTTCTG 8146
QY 6540 GATGGGCTCTTATAGCAATCTCTGAGAGCGGGTGAAGTCTGTTGA 6599
Db 8147 GATGGGCTCTTATAGCAATCTCTGAGAGCGGGTGAAGTCTGTTGA 8206

QY 6600 TGCCGGAAGCGAGAAATGCCCTATGGGCTGATATGACACCGGCTGTTTACTC 6659
Db 8207 TACCTGGAATCAAGAAATCCCATGGCTTTTCAATGACACTGCTGTTCCAGCTC 8266
QY 6660 AACGCTCAGTGAATGACATCGCTGTTGAGAGTCAATCTACCAATGTTGTGACTGGC 6719
Db 8267 AACGCTCAGTGAATGACATCGCTGTTGAGAGTCAATCTACCAATGTTGTGACTGGC 8326
QY 6720 CCCCAGGCGAGAGGCGATTAAGTGGCTACAGAGCGGCTTACCTGAGGGGCCCT 6779
Db 8327 CCCCAGGCGAGAGGCGATTAAGTGGCTACAGAGCGGCTTACCTGAGGGGCCCT 8386
QY 6780 GACTAATCTAAGGCGAGAACTGCGGCTATGCGGCTGCGGCGAGCGCTGACTGAC 6839
Db 8387 GACTAATCTAAGGCGAGAACTGCGGCTATGCGGCTGCGGCGAGCGCTGACTGAC 8446
QY 6840 GACGAGTCCGCTATACCTCAGATGTTACTTGAAGCGGCTGCGGCTGCTGAGCTGC 6899
Db 8447 GACTAGTCCGCTATACCTCAGATGTTACTTGAAGCGGCTGCTGAGCTGCTGAGCTGC 8506
QY 6900 GAGCTCCAGAGACTGACAGATGCTGATGCGGAGAGACCTTGCTGATCTGTGAAG 6959
Db 8507 GAGCTCCAGAGACTGACAGATGCTGATGCGGAGAGACCTTGCTGATCTGTGAAG 8566
QY 6960 GCGGGGAGCCAGAGAGAGAGCGAGGCTTACGGGCTTACGGAGGCTATGACTAGATA 7019
Db 8567 GCGGGGAGCCAGAGAGAGAGCGAGGCTTACGGGCTTACGGAGGCTATGACTAGATA 8626
QY 7020 CTCTGCCCCCTGAGGAGCCGCCCAACAGATTAAGTGAATGATTAACATCATG 7079
Db 8627 CTCTGCCCCCTGAGGAGCCGCCCAACAGATTAAGTGAATGATTAACATCATG 8686
QY 7080 CTCTCTCAATGTGTAGTCCGAGCAGATGATCTGCGAAGAGGTGATCTACCCG 7139
Db 8687 CTCTCTCAATGTGTAGTCCGAGCAGATGATCTGCGAAGAGGTGATCTACCCG 8746
QY 7140 TGACCCAGACACCCCTGAGGAGGCTGCTGAGAGAGAGCTGAGACACTGACGACAA 7199
Db 8747 TGATCCAGACACCCCTGAGGAGGCTGCTGAGAGAGAGCTGAGACACTGACGACAA 8806
QY 7200 TTCTGTGCTAGGCAATCATGATGATGCGCCCACTTGTGCGAAGAGATGCTGAT 7259
Db 8807 TTCTGTGCTAGGCAATCATGATGATGCGCCCACTTGTGCGAAGAGATGCTGAT 8866
QY 7260 GACTAATCTCTGCAATCTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 7319
Db 8867 GACTAATCTCTGCAATCTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 8926
QY 7320 GATCTACGGGGGCTGTACTGATGAGCCACTTGTACTGATCATGATCATGATCATG 7379
Db 8927 GATCTACGGGGGCTGTACTGATGAGCCACTTGTACTGATCATGATCATGATCATG 8986
QY 7380 CCATGCGCTTACGCAATTTTCACTCATAGTACTCTCCAGGTGATCAATGAGTGGC 9046
Db 8987 CCATGCGCTTACGCAATTTTCACTCATAGTACTCTCCAGGTGATCAATGAGTGGC 9096
QY 7440 TTCTATGCTCAGAGAACTTGGGGTACCGGCTTGGAGTCTGAGACATCGGGCAGAG 7499
Db 9047 TTCTATGCTCAGAGAACTTGGGGTACCGGCTTGGAGTCTGAGACATCGGGCAGAG 9106
QY 7500 TGTCCGCTTACGCTATGCTCCAGGGGGAGAGGCTCCACTTGTGGCAGTACCTCT 7559
Db 9107 TGTCCGCTTACGCTATGCTCCAGGGGGAGAGGCTCCACTTGTGGCAGTACCTCT 9166
QY 7560 CAAGTGGGAGTAAAGGAGCAAGCTCAAACTCACTCAATCCGCTGCTCCAGTTGA 7619
Db 9167 CAAGTGGGAGTAAAGGAGCAAGCTCAAACTCACTCAATCCGCTGCTCCAGTTGA 9226
QY 7620 TTTATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7679
Db 9227 TTTATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9286

RESULT 11
US-08-324-977-35

ADDRESS: Armstrong, Westernman, H
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

```

? ZIP: 20006
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.5 in., 1.44mb
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
? SOFTWARE: ASCII
? CREATOR: MICROSTAR INT'L
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,9777
FILING DATE: 18-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIORITY APPLICATION DATA:

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APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
Need Application Data

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/099,706
 ? FILING DATE: 30-JUL-1993
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/769,996
 ? FILING DATE: 02-OCT-1991

? PRIOR APPLICATION DATA: US 07/635,451
 ? APPLICATION NUMBER: 08-000000
 ? FILING DATE: 28-DEC-1990
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Stevens-Smith, Theresa M.
 ? REGISTRATION NUMBER: 36,281
 ?

REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 655-2930
TELEFAX: (202) 887-0357
TELEX: 440142

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: INFORMATION FOR SEQ ID NO: 35
:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 7863 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single

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Query Match	64.8%;	Score 5175.2;	DB 1;	Length 7865;
Best Local Similarity	91.8%;	Pred. No. 0;		
Matches 5468;	Conservative	0;	Mismatches 489;	Indels 0;
			Gaps	0.

QY 1800 CATGGCGCCTATTACGGCCTACTCCCMACAGCGCGAGGCTACTTGGCTGTCATCATCAC 1859
 |||||
 Db 1908 CCTGGGCCCATACGGCCTACTCCCAACAGCGGGGGGCTACTTGGTTGCATCATCAC 1967
 |||||
 QY 1860 TAGCCTACAGCGCGGACAGACAGGTCAGGGGAGGTCCAGGTCCTCCACGC 1919
 |||||

Db 1968 TAGCCTTACAGGGCGGAGACAGAACCCAGGTTCAGAGGAGAGGTTTCACACGC 2027

Cy 1920 AACCAATCTTTTCTGGCGACCTGCGTCAATGGCGTGTGTGGACGTGTCATATCGTGTC 1979

Db 2028 AACCAATCTTCTCTGGCGACCTGCGTCAAGCGGTGTGTGGACGTTTCACATGCTGC 2087

Qy	1980	CGGCTCAAGACCTTGGCCGCCCAAGGGGCCAATTCACCCAAATGTACACCAATGTGTGA	2039
Qy	2088	TGGCTCAAGACCTTACCCGCCCAAGGGGCCAATTCACCCAGATGTACAAATATGTGA	2147
Qy	2040	CCAGACCTGATGGCTGGCAAGCGCCGCCGGGCGGTTCTTGACACCATGCACCTG	2099

Db 2148 CCAAGACCTGTCGGCTGGGCCCAAGCCCCCGGGGGCGCTTCCTTGACACCATCACCTG 2207

QY 2100 CGGACGCTCGGACCTTACTTGGTCACAGAGGATGCCATGTCAATCCGGTGGCGCGGG 2159

Db 2208 TGGCAGCTCAGACCTTACTTGGTCACGAGACATGTGACGTCATTCGGGTGGCCCGGG 2267

[illegible][illegible]

QY 2340 GGGGCTCCCGGCTCTTTCACGGACAATCTGTCCTCCGGSCGTACCGCAATTCACAGT 2359
|||||
Db 2448 GGGGCTCCGGCTTTCACGGACAATCTATCCCCCGGSCGTACCGCAATTCACAGT 2507
QY 2400 GGGCATTCTACAGCCCCCTACTGTAAGGCGGCAAGACACTAAGTGTGGCGGTGGATGC 2459

Db 2508 GAGCCACCTACACGCTCCACTGCGACGGCAGAGTAATAAGTGGCGGTGCTATTC 2567

Qy 2460 AGCCCAAGGATATAGTGTCTTCTCTGAACCGGTCCGTCGGCGCACCTAGATTCCG 2519

Dp 2566 AGCCCAAGGATCAAGGTGCTCGTCTCTCAATCCGTCCGCTGCGCTACCTTAGGGATTGG 2627

Qy	2520 GGCCTATATGTCATAAGGCACATGGTATCGACCCTAACATCAGAAACGGGGATTAGACCAT 2579
Db	2628 GCCGTATATGTCATAAGGCACACGGTATTTGACCCCAACATCAGAATCTGGGGTAGAAGACCAT 2687

[illegible]

Dc	2748	CTCTGGGGGGCTTATGACATCATATATGTGATGAGTGGCCATTCAACTACTGACTGATAC	2807
Qy	2700	TATCTGGGCATCGGACAGTCTCTGGACCAAGCGGAGCGGCTGGAGCGGACTCGT	2759
Dc	2808	AATCTTGGGATCGGACAGTCTCTGACCAAGCGGAGCGGCTGGAGCGGCTTGTG	2867
Qy	2760	GTCTGCCACCGCTACGCCCTCCGGGATGCGTACCGGTGCACATCAACATTCGAGAGGT	2819
Dc	2868	GTCTGCCACCGCTACGCCCTCCGGGATGCGTACCGGTGCACACCCCAACATTCGAGAGGT	2927
Qy	2820	GGCTGTCTCCAGCACTGGAGAAATCCCTTTTATGCGAAAGCCATCCCATTCGAGACAT	2879
Dc	2928	GGCCCTGTCTAATACTGGAGAGATCCCTCTTATGCGAAAGCCATCCCATTCGAGACAT	2987
Qy	2880	CAAGGGGGGAGGAGGACCTATTTTGGCATTCGAAGAAATGTGATGGCTGGCGCG	2939
Dc	2988	CAGGGGGGAGGAGCATCTCATTTTCTGTATTCGAAGAAATGTGCGAGCGCTGGCGCG	3047
Qy	2940	GAAGCTGTCCGGGCTCGGACTCAATGCTGTAGCATATTTACGGGGCCTTGATGTACGT	2999
Dc	3048	AAACCTGTACGGGCTCGGAATCAACGCTGTGCGCTATTACCGGGGGCTCGATGTGCGGT	3107
Qy	3000	CATACCACTAGGGGAGAGAGTCATTGTGTGTACCAAGGAGGCGCTAATGAGCGGCTTAC	3059
Dc	3108	CATACCACTATGTGAGAGAGCTCTGTCTGTGCAACAGACGCTGTGATGAGCGGCTATAC	3167
Qy	3060	CGGCGATTTGTAGCTCACTGATGACATGCAATACATGTGTCAACCGAGAGAGTGCATTCAG	3119
Dc	3168	GGGCGACTTTGACACTAGTATGATGACATGATGACATGTGTCAACCGAGAGAGTGCATTCAG	3227
Qy	3120	CTTGAGACCCGACCTTACCACTTGTAGAGAGAGAGCGGTGCACAGAGCGGGGTGACGCTC	3179
Dc	3228	CTTGAGATCCCACTTACCACTTGTAGAGAGAGAGCGGTGCACAGAGCGGGGTGACGCTC	3287
Qy	3180	GCACGGCGAGAGCGAGACTGTTAGGGGCGAGATGGGCAATTTACAGGTTTGTGACTCCAGG	3239
Dc	3288	GCACGGCGGGGTGAGGAGCTGGACGGGGTGTAGAGAGGCAATCTACAGGTTTGTGACTCCGGG	3347
Qy	3240	AGAAAGGGGCGCCGGGGGCACTGTTGCATTCCTCGGGTGTGTGCGAGTCTGTACCGGGCGTG	3289
Dc	3348	AGAAAGGGGCGCCGGGGGCACTGTTGCATTCCTCGGGTGTGTGCGAGTCTGTACCGGGCGTG	3407
Qy	3300	TGCTTGTGACGAGCTACGACCGCGCCGCGAGACCTGATGTAGGTTGCGGGCTTACCTTAACAC	3359
Dc	3408	TGCTTGTGACGAGCTACGACCGCGCCGCGAGACCTGATGTAGGTTGCGGGCTTACCTTAACAC	3467
Qy	3360	ACCCAGGTTGCGCCGCTTGTGCCAGGAGCCATCGGAGTCTGTGGAGAGCGCTTTTACAGGCGCT	3419
Dc	3468	ACCCAGGTTGCGCCGCTTGTGCCAGGAGCCATCGGAGTCTGTGGAGAGCGCTTTTACAGGCGCT	3527
Qy	3420	CACCCATATAGAGCCCATTTCTTGTGCCAGACTTAAGCAGGCGAGAGACACTTCCCTA	3479
Dc	3528	CACCCATATATGATCACACTTCTTGTGCCAGACCAAGCGGAGAGAACAACTTCCCTA	3587
Qy	3480	CTGTGTACCATACAGGCTACGGGTGTGCCAGGAGGCTCAGGCTCAGCTCATCGTGGGA	3539
Dc	3588	CTGTGTACCATACAGGCAAGCAAGGTGTGCCAGGAGGCTCAGGCTCAGCTCATCGTGGGA	3647
Qy	3540	CCAAATGTGGAATGTCTCATACGGCTAAAGCTACGCTGTACAGGGCCAAAGCCCTCTCT	3599
Dc	3648	TCAAATGTGGAATGTCTCATACGGCTAAAGCTACGCTGTACAGGGCCAAAGCCCTCTCT	3707
Qy	3600	GTATAGGCTGGAGCGCTTCAAACGAGAGTTACTTACCAACACCCCATTAACCAATACAT	3659
Dc	3708	GTATAGGCTGGAGCGCTTCAAACGAGAGTTACTTACCAACACCCCATTAACCAATACAT	3767
Qy	3660	CATGCAATGCAATGTGGGTACCTGTGAGAGTGTCTACAGAGACCTGGGTCTGTAGGGGG	3719
Dc	3768	CATGCAATGCAATGTGGGTACCTGTGAGAGTGTCTACAGAGACCTGGGTCTGTAGGGGG	3827
Qy	3720	AATCTTAGAGTGTGGCGGGTATTCCTGTACACAGGAGCGTGTATTTGTGGGCG	3779

Db	3828	AGICTTTGCAGCTCTGCCCCGCTGATTGGCTGACCAACAGCAGCACTGTGTGTCATGTGGGTAG	3887
OY	3780	GATATCTTTGTCGGGAAGCGCCGCATCATCTCCGACAGGAAGTCTTTACCGGGAGTT	3839
Db	3888	GATTATCTTTGTCGGGAGCGCCGCATTTGTTCCCGACAGGAGCTTCTCTACCAAGAGTT	3947
OY	3840	CGATGAGATGGAAGAAGCGCCTCACACCTCCCTTCATCTGAAACAGSAGATCAGCTGCG	3899
Db	3948	CGATGAAATGGAAGAAGTGGCCTTGACCTCTCTTCATCTGACAGGAGATACACTGCG	4007
OY	3900	CGAATCTTCAACAGAAAGCAATCGGTTGGTGTGCAAAACAGCACCAACCAAGCGGAGCG	3955
Db	4008	CGACCAATTCAGAGAGAAGCGCTCGGGTTACTGCAACAGCGCCACCAACAGCGGAGCG	4067
OY	3960	TGCTGCTCCCTGGTGGAAATCCAAGTGGCGGACCTCGAAGCCCTTCTGGGCGAAGCAT	4015
Db	4068	TGCTGCTCCCTGGTGGAGTCCAAGTGGCGAGCCCTTGAGACATTTCTGGGCGAAGCAT	4127
OY	4020	GTGGAATTTCTACGCGGGATACATATTTAGAGGCTTGTCACACTCTGCGGCAAGCC	4077
Db	4128	GTGGATTTCTACGCGGGATACGTACTTAGAGGCTTATCCACTCTGCTGGAGACC	4187
OY	4080	CGCGATAGCACTAGTGGCATTCACAGGCTCTATCACAGCGCGCTCACCAACCCACACA	4133
Db	4188	CGCATATACATCATGATGAGCATTCACAGCCTTATACACAGCGCGCTCACCAACCAAG	4247
OY	4140	TACCTCTCTTTTAACATCTGGGGGGATGGTGGCGGCCAATTGTCCTCCAGCC	4199
Db	4248	TACCTCTCTTTTAACATCTGGGGGGATGGTGGCGGCCAATTGTCCTCCAGCC	4307
OY	4200	TGCTTCTGCTTTGCTAGGCGCGCGCATCGCTGAGCGGCTGTTGGACATAGGCTTGG	4255
Db	4308	CGCTTCTGCTTTGCTAGGCGCGCGCATCGCGGTGGTGGGACATAGGCTTGG	4367
OY	4260	GAAAGTGGTTGGATATTTTGGAGGTTATGGAGCAAGGGGTGGCAAGGCGCTGCTGGC	4317
Db	4368	GAAAGTGGTTGGACATTTCTGGCGGGTTATGGAGCAAGGATGGCGGCGCTGCTGGC	4427
OY	4320	CTTTAAGTTCATGAGCGGCGAGATGCCCTCCACCGAGAGACTTGGCTTAACCTACTCTGC	4377
Db	4428	CTTTAAGTTCATGAGCGGCGAGATGCCCTCCACCGAGAGACTTGGCTTAACCTACTCTGC	4487
OY	4380	TATCTCTCCCTGGCGGCTTATGCTGGGGGTGCTGCGACGATCTGCTGGGCA	4437
Db	4488	CATCTCTCTCTGGCGGCTTATGCTGGGGGTGCTGCGACGATCTGCTGGGCA	4547
OY	4440	CGTGGGCCCAAGGGAGGGGGCTGTGCACTGATTAACCGGCTGATAGCTTCCCTTCGGG	4497
Db	4548	CGTGGGTCCGAGAGGGGGGCTGTGCACTGATTAACCGGCTGATAGCTTCCCTTCGGG	4607
OY	4500	GGGTAAACCAAGCTCCCCCAGCACTATGTCTCTGAGAGGAGCCCTTCACACAGTGTCA	4557
Db	4608	GGGTAACTCATGTTTCCCCCAGCACTATGTCTCTGAGAGGAGCCCGCAGCGGCTGTAC	4667
OY	4560	TCAGATCTCTCTAGTCTTACCATCTACTCACTGCTGTAAGAGGCTTACCACATGTGATCA	4617
Db	4668	TCAGATCTCTCTACACCTTACCATCTACTCACTGCTGTAAGAGGCTTACCACATGTGATTA	4727
OY	4620	CGAGGACTCTCCAGCACTGCTCGGGTCTGTGCTAAGAAATTTTGGGATTTGGATATG	4677
Db	4728	TCAGAGCTCTCCACACCTGTTCCGGCTCGAGGCTAAGGATTTTGGGACTGATATG	4787
OY	4680	CACGCTGTGACTGATTTCAAGACTGGCTCAAGTCCAGTCTCTGGCGGATTTGGCGGG	4737
Db	4788	CACGCTGTGACTGACTTTCAAGACTGGCTCAAGTCCAGTCTCTGGCGGATTTGGCGGG	4847
OY	4740	AGTCCCTTCTTCTCATGTCAACAGTGGGTACAAGGATCTGGCGGGGCGAAGCATCAT	4797
Db	4848	AGTCCCTTCTTCTGTGTCACAAGGCGGTACAAAGGATCTGGCGGGGAGCAGCATCAT	4907
OY	4800	GCAACCACTGCTCCATGTGGAGCAACATACCGGAGATGTGAAAAAGGTTTCCATGAG	4857
Db	4908	GCAACCACTGCTCCATGTGGAGCAACATACCGGAGATGTGAAAAAGGTTTCCATGAG	4967

QY	4860	GATGCTGGGGCCCTAGAACCTCTGTAGTAACACGTGGCATGTGACATTTCCCATTAACGGCTA	4913
Db	4968	GATGCTGGGGCCCTAGAACCTCTGTAGTAACACGTGGCATGTGACATTTCCCATTAACGGCTA	5027
QY	4920	CACCACGGGGCCCTGACACGGCCCTCCCGGGCCCAATTATTTCTAGGGCGCTGTAGCGAGT	4979
Db	5028	CACCACGGGGCCCTGACACGGCCCTCCCGGGCCCAATTATTTCTAGGGCGCTGTAGCGAGT	5087
QY	4980	GGCTGCTGAGAGGTACGTGGAAGTTACGGGGGTGGGGATTTTCCACTACGTGACGGGCAT	5039
Db	5088	GGCCGGCTGAGAGGTACGTGGAAGTTACGGGGGTGGGGATTTTCCACTACGTGACGGGCAT	5147
QY	5040	GACCACGTAGAACGTAAAGTGGCCCGTGTAGGTTCCGGCCGGCCCGCAATTTCTTACAGAGT	5099
Db	5148	GACCACGTAGAACGTAAAGTGGCCCGTGTAGGTTCCGGCCGGCCCGCAATTTCTTACAGAGT	5207
QY	5100	GGATGGGGGTGCGTTGACACAGGTACGCTTCACAGTCCAAACCCCTCTACGGGAGAGGT	5159
Db	5208	GGAGCGAGTGGGTGTGACACAGGTACGCTTCGAGTCCGCGGTGACAGCTCTCTCTACGGGAGAGT	5267
QY	5160	CACATTCCTGATCGGGCTCATCATACCTGTTGGGTACACAGTCCCATCGAGCCGA	5219
Db	5268	TACATTCAGAGTGGGTCTCAACCATACCTGGTTGGGTACAGGTACCATCGAGCCGA	5327
QY	5220	ACGGAGGTAGCAGTGGCTCATCTCCATNGTCACACGACCCCTCCCACTTACGGGGAGAC	5279
Db	5328	ACGGAGGTAGCAGTGGCTCATCTCCATNGTCACACGACCCCTCCCACTTACGGGGAGAC	5387
QY	5280	GGCTTAAGCGTAGGCTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCATAGCTAGCA	5339
Db	5388	GGCTTAAGCGTAGGTTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCATAGCTAGCA	5447
QY	5340	GCTGTCTGCGCTTCCCTTGAAGGCACACATGCAATACCGTCAATGACCTCCCGAGCGTGA	5399
Db	5448	GTTGTCTGCGCTTCCCTTGAAGGCACACATGCAATACCGTCAATGACCTCCCGAGCGTGA	5507
QY	5400	CCTCATCGAGGCCAACCTCCTGTGGGGGACAGAGTAGGGGGGAAACATACCCGGCTGA	5459
Db	5508	CCTCATCGAGGCCAACCTCCTGTGGGGGACAGAGTAGGGGGGAAACATACCCGGCTGA	5567
QY	5460	GTCGAAATAAGTACTATTTTGGACCTTTCGAGCGCGCTCCCAAGGGGAGAGATGA	5519
Db	5568	GTCGAGAACAGGTGGTGGTACCTTCGGACTTTTCGACCCGCTTCGAGGGAGAGATGA	5627
QY	5520	GAGGGAATATCCCTTCCTCCGGCGAGATCCTGCGGAGGTCCAGAAATTCCTTCGAGCAT	5579
Db	5628	GAGGGAATATCCCTTCCTCCGGCGAGATCCTGCGGAGGTCCAGAAATTCCTTCGAGCAT	5687
QY	5580	GCCCATATGGGCGAGCCCGGATTAACAACCTCCACATGTTAGAGTCTCTGGAAGAGCCGGA	5639
Db	5688	GCCCATATGGGCGAGCCCGGATTAACAACCTCCACATGTTAGAGTCTCTGGAAGAGCCGGA	5747
QY	5640	CTACGTCCCTCACTGTGTACACGAGGTGTCCATTGCCCGCTGCCAAGGCCCTCCGATACC	5699
Db	5748	CTACGTCCCTCCGATGTGTACACGAGGTGTCCCGTGGCCACCTATCAAGGCCCTCCGATACC	5807
QY	5700	ACCTCCACGGAGGAAGAGAGCGGTGTCTCGTGAAGATCATACCGATGCTCTCGCCCTGAGC	5759
Db	5808	ACCTCCACGGAGGAAGAGAGCGGTGTCTCGTGAAGATCTCTCGATGCTCTCGCCCTGAGC	5867
QY	5760	GGAGCTGCCAACAAGACTTGGCAGCTCCGATGCTGGCCGTGGACAGCGGACGGC	5819
Db	5868	GGAGCTGCCACTAAGACTCTGGCAGCTCCGATATCGAGCTGTGACAGCGGACGGC	5927
QY	5820	AACGGCCCTCTCTACACAGCCCTCCGACGACGGGACAGCGGGGATTCGAGCTTGAGTCTGA	5879
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US-08-384-616-35
; Sequence 35, Application us/08384616
; Patent No. 5847101
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FURE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
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FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIORITY APPLICATION DATA:
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FILING DATE: 31-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 687-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 7863 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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US-08-384-616-35
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Db 6408 GGAAGCTGTGAAGTGAAGCGCGCTTAAACCAATCCGCTCCGCTGTGAAGAGACTT 6467
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Db 7788 TGCCGAGCCCGGCTTGTGTTGTTGCTTACTCTACTCTTCTGTAAGGGGTAGCATCTA 7847
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Db 7848 CTTGCTCCCAACCGA 7863

RESULT 13
US-08-904-686A-35
Sequence 35: Application US/08904686A
Patent No. 5998130
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mclelland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 35:

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SEQUENCE CHARACTERISTICS:

LENGTH: 7863 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: CDNA FROM GENOMIC RNA

NAME/KEY. CDS

WAGLE/KEY:	CDS
LOCATION:	1

DOCHILION. 1..../B003

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2 ENDORD.
NAME/KEY: misc_feature

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LOCATION: 1..7863

OTHER INFORMATION:

OTHER INFORMATION: SEQ ID NO: 1"

3-904-686A-35

US-08-904-686A-35

Query Match	64.8%	Score 5175.2	DB 2	Length 7863
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Best Local Similarity 91.8%; Pred. No. 0;

Matches 5468; Conservative 0; Mismatches 488; Indels 0; Gaps 0;

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QY	1860	TACCTTCACAGCCCGGGACAGGACACAGGTGAGGGGGAGGTCCAGGTGGTCTCCACCCG	1919
Db	1968	TACCTTTACAGCGCGGGACAAAGAACAGGTGAGGGAGAAAGGTTAGGTGGTTTCCACCCG	2027
QY	1920	AACACATCTTTCCTTGGCAGCTGGCTGAATGGCGTGGTTGGAGCTCTCATATGATGTCG	1979
Db	2028	AACACATCTTTCCTTGGGAGCTGGGTCAAGGGCGCTGGTTGGAGCGCTTTACCATGGTGG	2087
QY	1980	CGGCTCAAAAGACCCTTGCCGGGCCCAAGGGGCCAATCACCCAAATGTACACCAATGTGGA	2039
Db	2088	TGGCTCAAAAGACCTTATGCGCGCCCAAGGGGGCAATCACCCAGATGTACATATGTGGA	2147
QY	2040	CCAGGACCTGTGGGTGGCCAAAGCCCGCCCGGGGCGCGTCTTGACACATGACACTG	2099
Db	2148	CCAGGACCTGTGGGTGGGCCCAAGCCCGCGGGCGGTCTTGACACATGACACTG	2207
QY	2100	CGGAGCTGGAGACTTTACTTGGTACAGAGGATGCGATGTCATTTCCGTGGCGCGCG	2159
Db	2208	TGGAGCTGAGACCTTTACTTGGTACAGAGATCTGTACGTCAATTCGGGTGGCGCGCG	2267
QY	2160	GAGGAGACAGAGGGGAGGAGCTACTCTCCCGCCAGGCGCGCTCTCATCTTGAAGGAGCTTTC	2219
Db	2268	GAGGAGACAGAGGGGAGGAGCTCTCTCCCGCCAGGCGCTCTCTCATCTTGAAGGAGCTTTC	2327
QY	2220	GAGGCGGTCCACTCTCTGTGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCCGTGTG	2279
Db	2328	GAGGTGTCCACTCTCTGTGCCCTTGGGGAGCGCTGTGGGCACTTTCGGGCTGCCGTGTG	2387
QY	2280	CACCCGAGGGGTTGGCCAAAGGCGGTGAGACTTTTACCCGTCCAGTCTATGAAACACATAT	2339
Db	2388	CACCCGAGGGGTTGCCAAAGGCGGTGAGACTTTTGGCCGTAAAGTCCATGGAATACATAT	2447
QY	2340	GCGGTCCCGGCTTTCAGGAGACACTGTCCCTCTCGGCGCTACCGCAGACATTTCCAGGT	2399
Db	2448	GCGGTCTCCGCTTTCAGGAGACACTGTCCCTCCCGGCGCTACCGCAGATATTTCCAGGT	2507
QY	2400	GAGCCATCTACAGGCCCTACTGTAGCGGCAAGAGACACTAAGGAGCGCGGTGGCTATGTC	2459
Db	2508	GAGCCACCTACAGGCTTCCACTGTGACGGGCGCAAGAGTACTAAATGGCCGCTGATATGTC	2567
QY	2460	AGCCCAAGGATTAAGGTGCTTGTCTGTGAACCCGTCCGTCGCCGCCACCTAGGTTTCGG	2519
Db	2568	AGCCCAAGGATTAAGGTGCTTGTCTGTGAACCCGTCCGCTTCCGCTACTTAAGGTTTCGG	2627
QY	2520	GAGCTATATGTCTAAGGACACATGTATGCACACTTAACATCGAAACCGGGGTAAAGACCAT	2579
Db	2628	GAGCTATATGTCTAAGGACACAGGATTTAGACCCCAACATCGAATCTGGGTAAAGACCAT	2687
QY	2580	CACCACGGGTGCCCCATCACTACTCCACTATGACAAATTTCCTTGCCACAGGTGGTTG	2639

Db	2688	TACCACGAGGGCCCCCGTCACATCTTACTACTTAGGCAAGTTCTTGGCGATGGTGG	2747
Qy	2640	CTCTGGGGGGGCGCTAAGACATATATAATATGTGATGAGTGGCCACTCAACTGACGACAC	2699
Db	2748	CTCTGGGGGGGCGCTTAAGACATATATAATATGATGATGGTGCATTCAACTGACTCGACTTC	2807
Qy	2700	TATCTGTGGGANTGGACAGCTCTGAGACAGCGGAGACGGCTGGAGCGCTACTGCTGCT	2759
Db	2808	AATCTTGGGCATGGCAGACAGTCTCTGGACCAAGCGGAGACGGCTGGAGCGCTTGTGCT	2867
Qy	2760	GCTGGCCACCGCTACGCGCTCCGGGATCGGTGACCGTGCACATCCAAACATAGAGAGGT	2819
Db	2868	GCTGCGCACCGCTACGCGCTCCGGGATCGGTGACCGTGCACACCCCAACATCGAGAGGT	2927
Qy	2820	GGCTCTGTCCAGCAGCTGAGAAATCCCTTTATGGCAAGGCCATCCCATGGAGCAAT	2879
Db	2928	GGCCCTGTCTAATACTGGAGAGATCCCTCTATGGCAAGGCCATCCCATGGAGCAAT	2987
Qy	2880	CAAGGGGGGGGAGGACCTCATTTCTGSCATTTCCAGAGAAATGTGATGAGTGGCGCG	2939
Db	2988	CAGGGGGGGAGGACATCTATTTTCTGTCAITTCAGAGAAATGGGACGAGCTGGCGCG	3047
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Qy	3000	CATACCACTAGGGGAGAGTGAATGTGTGTAGCAAGGACGCGCTATATGACGGGCTTAC	3059
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Qy	3120	CCTGAGCCGACCTTACCATTTAGAGCGACGCGCGCTGGCACAAGACCGGCTGTACGCTTC	3179
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Qy	3240	AGAGCGGCGCTCGGGGATGTGTGATTCCTCGGTTCTGTGCGAGGTGATATACCGGGCTG	3299
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Qy	3300	TGCTTGTAGAGACTACGCGCGCGAGACCTCATTTAGTTGCGGGCTTACTATAACAC	3359
Db	3408	TGCTTGTGTAGAGACTACCGCGCGAGACCTCGGTTAGTTGTGGGGCTTACTGTATACAC	3467
Qy	3360	ACGAGGTTGCGCGTCTGCGAGAGACCATGTGAGTTCTGGGAGAGCGCTTTCACAGAGCT	3419
Db	3468	ACGAGGTTGCGCGTCTGCGAGAGACCACTGAGTTCTGGGAGAGGTCTTTCACAGAGCT	3527
Qy	3420	CACCCATATAGACGCCCATTTCTTGTCCAGACTAAGCAGGCGAGAGACACTTCCCTTA	3479
Db	3528	CACCCATATAGATGACACTTCTTGTCCAGACCAAGCAGGCGAGAGACAACTTCCCTTA	3587
Qy	3480	CCTGATGTACATACAGAGTACGGGTGTGGCGCGAGGACTCAGGCTCAGCTTCATGCGGGA	3539
Db	3588	CCTGATGTACATACCAACCCAGCGTGTGGCGCGAGGCTTAGGGCCCCACTCTCATCATGGGA	3647
Qy	3540	CCAAATGTGAGATGTCTCATAGGCTTAAGCCTTACGCTGACGAGGCGCAACGCCCTGCT	3599
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Db 3768 CATGGCATGATGTCGGCTGACCTGAGAGTGTCTCACTAGCACTGGCTGTGAGCGG 3827
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Db 3828 AATCCTTGAGCTTGGCCCGGCTATTGCTCTACAAAGGCGAGGTGTCTATTGGGCTAG 3887
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Db 3888 GATTATCTGTCCGAGAGCGCGGCATGTTCGCCAGAGGAGTCTTCTTACAGAGATT 3947
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Db 4488 CATCTCTCTCTGCGCGCCCTAGTGTGCTGGGTGCTGAGCGAGGATGCTGCGGCA 4547
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QY	5880	CTTCTGCATGCCCCCTTTGAGGGGGGGGGCCGGGGATGCTCCGATCTCAAGCCAGCCGGGCTTGG	5939
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QY	5940	GTCATCCGTAAGGAGAGGAGCTAGTAGGAGCACTGCTGCTGCTCGATGTCCTTACACATG	5999
Db	6048	GTCATCCGTAAGGAGAGGAGCTAGTAGGAGTGTGCTGCTGCTCAATGATGCTTACACATG	6107
QY	6000	GACAGGCGCCCTATATACGCGATGCGCTGCGGAGGAACGCAAGCTGCCCATCATATGACACT	6059
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QY	6180	CGTGCTCAAGAGATGAAAGGCGAAGGCGTCCACACTTAAGCTTAACACTTCTATCCGTGA	6239
Db	6288	CGTGCTCAAGAGATGAAAGGCGAAGGCGTCCACAGTTAAGCTTAACACTTCTATCCGTGA	6347
QY	6240	GGAAGCTGTAGCTGACGGCCCCACATTTGCGCCAGATCTAAATTGSGCTATGGGGCAA	6299
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QY	6300	GGAGGTCGGGAACTATCCAGCAAGGCGGTAAACCAATCCGCTCCGCTGTGGAAGACTT	6359
Db	6408	GGAGGTCGGGAACTATCCAGCAAGGCGGTAAACCAATCCGCTCCGCTGTGGAAGACTT	6467
QY	6360	GCTGGAAGACACTGAGACACCAATTTGACACACCAATCATGCGCAAAAAATGAGGTTTTCTG	6419
Db	6468	GCTGGAAGACACTGAGACCAATTTGACACCAATCATGCGCAAAAAATGAGGTTTTCTG	6527
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Db	7308	CTCTGGCTTAGGCAACATTTTATATGATGCGCCACTTGTGGCAAGATGATCTGAT	736
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RESULT 14
 US-09-315-850-35
 ; Sequence 35. Application US/09315850
 ; Patent No. 6217872
 ; GENERAL INFORMATION:
 ; APPLICANT: OKAYAMA, Hiroto
 ; APPLICANT: FUKU, Isao
 ; APPLICANT: MORI, Chisato
 ; APPLICANT: TAKAMIZAWA, Akahisa
 ; APPLICANT: YOSHIDA, Itao
 ; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMICS
 ; TITLE OF INVENTION: CNA AND ANTIGEN POLYPEPTIDE
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Armstrong, Westerman, Hattori, McLealand &
 ; ADDRESSEE: Naughton
 ; STREET: 1725 K St., N.W. Suite 1000

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-AUG-1997
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mclelland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 9007036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 7863 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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NAME/KEY: CDS
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US-09-315-850-35

Query Match 64.88: Score 5175.2: DB 4: Length 7863;
Best Local Similarity 91.88: Pred. No. 0;
Matches 5468: Conservative 0: Mismatches 488: Indels 0: Gaps 0:

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Qy	6240	GGAAAGCTGTAAAGTGAAGCGCCCAACTTGGGCGAAGTCTAAATTTGGCTATGGGGCAA	6299
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Qy	6300	GGAGCTCCGGAACCTATCCAGCAAGGCGTTAAACACATCCGCTCCGTGTGAAGAGCTT	6355

Db	6408	GGAGCTGCGGAACTCTATCCAGCAAGGCCGTTAACCACATCCACTCCGCTGGGAAGGACTT	6467
Qy	6360	GCTGGAAGACACTGAGACACACATTTGACACACCATCATGCGAATAAATGAGGTTTTCTG	6419
Db	6468	GCTGGAAGACACTGTGACACCATTTGACACACCATCATGGAATAAATAAGGTTTTCTG	6527
Qy	6420	CGTGCACACAGAAAGGGGGGCGCGCAAGCCAGCTCGCCTTATCGTATTTCCAGATTTGGG	6479
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Qy	6480	GGTTCGTCTGTGGAGAAAATGGCCCTTTACGATGTGGTCTCCACCCTCCCTCCAGGGCGT	6539
Db	6588	AGTCCGTGTATGGAGAAAGTGGCCCTCTATGATGGGTCTCCACCCTTCTCCAGGTCTG	6647
Qy	6540	GATGGGCTCTTCATACGATTCACATACCTCTCTGGACACGCGGGTGAATTCCTGGTGA	6599
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Qy	6600	TGCTCGAAGACGAAAGAAATGCCCCCTATGGGCTTCGATATGACACCCGCTGTTTGAATC	6659
Db	6708	TACCTGGAATAATCAAGAAAAACCCCATGGGCTTTTATATGACACTCGCTGTTTGAATC	6767
Qy	6660	AACGGTCACTAGATATACATCCGTTGTGAGAGTCAATCTACAAATGTTGTACTGGC	6719
Db	6768	AACGGTCAACGAAACGATCCGTTGTGAGAGTCAATTTCCAAATGTTGTACTGGC	6827
Qy	6720	CCCCGAGCCAGACAGCCCATTAAGTGTCCGTCACAGAGGGGGCTTTCATCGGGGGCCCCCT	6779
Db	6828	CCCCGAGCCAGAGAGGCCCATTAATAATGCTTCACAGAGCGGCTTTATATCGGGGGCTCT	6887
Qy	6780	GACTAATTTCTAAAGGCGCAGAACTCGCGCTATCGCCGGTGGCGCGAGCGGTGTACTGAC	6839
Db	6888	GACTAATTTCAAAAGGCGCAGAACTCGCGCTTATCCCGGTGGCGCGAGCGGTGCTAC	6947
Qy	6840	GACCACTGGCGGTATATACCTTCACATGTTACTTGAAGGGCGGTGGGGGCTGTCCAGCTGC	6899
Db	6948	GACTATGCTGGGTATACACCTCTCAATGTTTACTTGAAGGCTCTTCAGGCTGTCCAGCTGC	7007
Qy	6900	GAAGCTCCAGSACTGCAAGATGCTCTGTATGCGGAGACGACTTGTTCGTTATCTGTGAAG	6959
Db	7008	GAAGCTCCAGSACTGCAAGATGCTCTGTGAAGGAGACGACTCTGTATGTGTGAAG	7067
Qy	6960	CGCGGGGACCCCAAGAGACGAGGGGAGACCTTACGCGGCTTCAGGAGGCTATGACTAGATA	7019
Db	7068	CGCGGGAAACCCAAAGAGAGGACCGCGAGACCTTACGAGCTTTCAGGAGGCTATGACTAGATA	7127
Qy	7020	CTTGGCCCCCTGGGGACCCGCCCAACCAAGATTCGACTTGGAGTTATATACATCATG	7079
Db	7128	CTTGGCCCCCTGGGGACCCGCCCAACCAAGATTCGACTTGGAGCTTATATACATCATG	7187
Qy	7080	CTTCCGTCGAATGTGCAGTCGCGGCGCAGATGCGATGTGGCAAAAGGGTATATCTACACCG	7139
Db	7188	TTTCTTCGAATGTGTGCGTGGCGCCACGATGCGATAGGCCAAAGGGTATATCTACACCG	7247
Qy	7140	TGACCCCAACACCCCCCTTGGGCGGGCTGCGGTGGGAGACGCTAGACACATCTCAGTGCA	7199
Db	7248	TGATGCCACACCCCCCTTAGACGCGGTGGTGGGAGACGCTAGACACATCTCAGTTTA	7307
Qy	7200	TTCCTGCGTAGGCAACATCATATGATGTGGCGCCACCTGTGGGCAAGGATGATCTGAT	7259
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Qy	7260	GACTGATTTTCTTCCATCTTTCAGTCAGAGAAACAATTGAAAAAGCCCTGATTTGCA	7319
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Db	7488	CGATGGCCTTAGGCCATTTTACTCTCCATATGTACTCTCCAGGTGAAATATAGGGTGGC	7547

Oy	7440	TTTATGCGCTCAGGAAACTTTGGGTACCGCCCTTGCAAGTCTGAGACATCGGGCCAGAG	7459
Db	7548	TTTATGCTCAGGAAACTTTGGGGTACCACCCCTTGCAAGTCTGAGACATCGGGCCAGAG	7607
Oy	7500	TGTCGGCGCTAGGCTACTGTGCCAGGGGGGAGGCGCTGCCACTTGtGGCACTACCTTT	7558
Db	7608	CGTCCGGCGCTAGGCTACTGTGCCAGGGAGGAGGCGCGCACTTGtGGCAAACTACCTTT	7667
Oy	7560	CAACTGGGCACTAAGAGACCAAGCTCAAACTCACTCCATCCGGCGCTCCCACTTGA	7619
Db	7668	CACTGGGCACTAATAAACCAAACTTAACTCACTCCAACTCCGGCGCTCCCGGCTGA	7727
Oy	7620	TTTATCCAGCTGGTTCGTTGCTGTGTACAGGGGGGAGACATATACAGCTGTCTCG	7679
Db	7728	CTTGTCGGCGGTTCGTTCTCTCTGTGTACAGGGGGGAGACATATACAGCTGTCTCG	7787
Oy	7680	TGCCGAGCCCGCGTGTTCATGTGAGCCCTACTCTACTTCTGTAGGGGTAGGCATCA	7739
Db	7788	TGCCGAGCCCGGTGTGTTCATGTGAGCCCTACTCTACTTCTGTAGGGGTAGGCATCA	7847
Oy	7740	TCTACTCCCAACCA 7755	
Db	7848	CTTGCTCCCAACCA 7863	

```

ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..9030
OTHER INFORMATION: /note="sequence = 333 - 9362 of
FEATURE:
NAME/KEY: CDS
LOCATION: 1..9030
US-08-324-977-13

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Db 3675 GGGCCACCTACACGGCTCCCACTGGCAGCGGCAAGTACTAAAGTCCGGCTGCATATGC 3734

OY	2460	AGCAAGGATATNAGTGGTTCTCCGTGAACCGTCGCCGCACCCTTAAGTTTCG	2519
Db	3735	AGCCCAAGGGTACAAGTGCTGTCTCCTCATTCGTCGCTACCTTAGGGTTGG	3794
OY	2520	GAGCTATATGTCTAAGGCACATGGTATCGAACCTTAACATCAGAACGGGGTAA	2579
Db	3795	GCGCTATATGTCTAAGGCACACGGTATTGACCCCAACATCAGAACTGGGGTAA	3854
OY	2580	CACACGGGTGGCCCCATCACGTAATCCACTATGGCAATTTCTTGGCCAGGGTGG	2639
Db	3855	TACACAGGGGCCCCCTCATACACTCTACCTTAGGCAAGTTCTTGGCGATGGGTGG	3914
OY	2640	CTCTGGGGGGCCCTATACATCATATAATATGATGATGATGGCCACTACACTGAC	2699
Db	3915	CTCTGGGGGGCCCTATATGACATCATATAATATGATGATGATGATGATGATGATG	3974
OY	2700	TATCTGGGATATGGCAACATCCTCTGGACCAAGCGGAGACGGCTGGAGGGCACT	2759
Db	3975	AATCTTGGGCACTGGCAACATCCTGGACCAAGGGAGAGCGCTGGAGGGCGCTTGT	4034
OY	2750	GCTCGCACCGCTACGSCCTCCGGGATCGGTACCGGTGCACATCCAAATCGAGA	2819
Db	4035	GCTCGCACCGCTACGSCCTCCGGGATCGGTACCGGTGCACACCCAACATCGAGA	4054
OY	2820	GGCTCTGCGCAGCATGGAAAAATCCCTTTATGGCAAGGCATCCCATCGAGACAT	2879
Db	4095	GGCCCTGTCTAATCTGGAAGATCCCCTTCTATGGCAAGGCATCCCATTTGAAGCAT	4154
OY	2880	CABGGGGGAGGACCTCATTTTTGTGCCATTCOAAGAAATGTATGATGATGATGATG	2939
Db	4155	CAGGGGGGAGGAGCATCTCATTTTTGTGTCAATCOAAGAAAGTGCAGAGATCGCGC	4214
OY	2940	GAACTGTCCGGCCTCGGACTCATATGCTGTAGACATTTACCGGGCGTTAGTACCGT	2999
Db	4215	AAACTGTCAAGCCTCGGATTCACACGCTGTGGGTATTTACGGGGGCTGATGTCTGT	4274
OY	3000	CATACCACTAAGCGAGACGTATTTGTGCTAGCACAGACGCTCTAATAGCGGCTTTAC	3059
Db	4275	CATACCACTAATCGAACCTCGTTGTGCGTACMACAGACGCTCTGATAGACGGCTATAC	4334
OY	3050	CGGGAATTCGACACTGATATCGACACTGATATGATGTACACCAAGACAGTGCAGTTGAC	3119
Db	4335	GGGGAGCTTTGACCTATGATTCAGACTGTAACATGTGTACCCACAGACAGTGCAGTTGAC	4394
OY	3120	CCTGACCCGACCTTACACATTGAGACAGACCGTGGCCACAAGACGGGTGTACGCTC	3179
Db	4395	CTTGGATTCACCTTTCACCAATTGAGACAGACCGTGGCCACAAGACCGTGTCCGCTC	4454
OY	3180	GCACGCGGAGGACAGCATGTGTAGGGGAGAGATGGGCATTTACAGTTTGTATCTACAG	3239
Db	4455	GCAGGGGGGGGTGAGCATGGACAGGGGTAGGAAGGCATCTACAGTTTGTATCTACAG	4514
OY	3240	AGAAAGCGCCCTCGGGCATGTTTCATTCCTCGTCTGTGCGAGTGTCTATGACGGGGCTG	3299
Db	4515	AGAAAGCGCCCTCGGGCATGTTTCATTCCTCGTCTGTGAGTGTCTATGAGCGGGGCTG	4574
OY	3300	TGCTTGTGACAGGCTCAGCGCCCGCAGACCTAGTTAGTTGCGGGCTTACTAAACAC	3359
Db	4575	TGCTTGTGACAGGCTCAGCGCCCGCAGACCTGTTAGTTTGGCGGCTTACTAAACAC	4634
OY	3380	ACCAAGGTTGGCCCTCTGCGCAGACCATCTGGAGTTCTTGGGAGAGCGTTTACAGGCT	3419
Db	4635	ACCAAGGTTGGCCCTTTGCGCAGACCATCTGGAGTTCTTGGGAGAGTTTACAGGCT	4694
OY	3420	CACCCACATAGACGCCCATTTCTTGTCCAGATTAAGCAGGAGGAGACACTTCCCTA	3479
Db	4695	CACCCATPATATGATCAGACCTTCTGTGCCAGACCAAGCAGGAGGAGAACACTTCCCTA	4754
OY	3480	CTGTGTACATACACAGGCTACGGGTGGCGCAGAGGCTACAGCTCTCATCTGTGGGA	3539
Db	4755	CTGTGTACATACCAAGCACGGGTGGCGCAGAGGCTACAGGCTCTCATCTGTGGGA	4814
OY	3540	CCAAATGTGAAGTGTCTCATAGCGCTAAAGCCCTACGCTGACAGGGCCCAACGCCCTCT	3599

[illegible]

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Q	4680	CACGGTGTGACATGATTTCAAGACCTGGCTCCAGTCCAGGCTCCTGCCGATTTGCCGG	4739
D	5955	CACGGTGTGACATGATTTCAAGACCTGGCTCCAGTCCAGGCTCCTGCCGAGCTTACTGG	6014
Q	4740	AGTCCCTTCTTCTCATGTGCAACCTGGGTACAAAGGAGATCTGGGGGGGACAGGCAATCAT	4799
D	6015	AGTCCCTTCTTCTCGTGGCAACGGGGGTACAAAGGAGATCTGGGGGGGACAGGCAATCAT	6074
Q	4800	GCAAAACCACTGCCATGTGTGAGACACAGATACCCAGACATGTGAAAAAAGTTTCATAG	4859
D	6075	GCAAAACCACTGCCATGTGTGAGACACAGATACCCAGACATGTGAAAAAAGTTTCATAG	6134
Q	4860	GATGTGTGGGCTCATAGAACCTGTGTAAACAGTGTGCATATGAAACATTTCCCATTAACGGTA	4919
D	6135	GATGTGTGGGCTCATAGAACCTGTGTAAACAGTGTGCATATGAAACATTTCCCATTAACGGTA	6194
Q	4920	CACCACGGGCCCCGACACGGCCCTCCCCGGCGCAATTAATTCAGGGCGCTGTGGCGGT	4979
D	6195	CACCACGGGCCCCGACACGGCCCTCCCCGGCGCAATTAATTCAGGGCGCTGTGGCGGT	5254
Q	4980	GGCTGCTGAGAGTACGTGAGGTTACGGGGTGGGGATTTTCCACTACGTACGGGCAT	5039
D	6255	GGCGCGTAGAGAGTACGTGAGGTTACGGGGTGGGGATTTTCCACTACGTACGGGCAT	6314
Q	5040	GACCACTGACAAGTAAAGTGGCCGTTGAGGTTCCGGGCCCCGCAATTCCTACAGAGT	5099
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Q	5100	GGATGGGGTGGGTTGACAGGTACGCTCCAGCGTGCAAACCCCTCTCTACGGGAGAGT	5159
D	6375	GGAGGGAGTGGGTTGACAGGTACGCTCCAGCGTGCAAACCCCTCTCTACGGGAGAGT	6434
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D	6435	TACATTCGAGGTCCGGCTCAACCAATACCTGGTGGGTCAAGCTCCCATCGAGCCGA	6494
Q	5220	ACCGAGGTACAGTGTCTACTCTCAATGTCTACACGACCCCTCCCATTAAGCGCGAGAC	5279
D	6495	ACCGAGGTACAGTGTCTACTCTCAATGTCTACACGACCCCTCCCATTAAGCGCGAGAC	6554
Q	5280	GGCTAAGGTAGGCTGGCCACGGGAGTCTCCCCCTCTTGGCAGACTCATACGTAGCA	5339
D	6555	GGCTAAGGTAGGCTGGCCACGGGAGTCTCCCCCTCTTGGCAGACTCATACGTAGCA	6614
Q	5340	GCTGCTCGGCTTCCTTGAAGGCAATCACTACCCGCTCATGTACTCCCGGAGCGCTGA	5399
D	6615	GTTGTCTCGGCTTCCTTGAAGGCGACATGCACTACCCACATGTCTCCGGAGCGCTGA	6674
Q	5400	CCTCATGAGGCCAACCTCCTGTGGCGGACAGAGATGCGCGGAAACATCACCCGCTGGA	5459
D	6675	CCTCATGAGGCCAACCTCCTGTGGCGGACAGAGATGCGCGGAAACATCACCCGCTGGA	6734
Q	5460	GTCACAATAATGAGTAAATTTTGGACTTTTCGAGCGGCTCCACAGCGAGAGAGATGA	5519
D	6735	GTCGAGAACAAAGTGTGATGCTCTGAGACTTTTTCGAGCGGCTTCGAGCGAGAGAGATGA	6794
Q	5520	GAGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGAGTCCAGAAATTCCTCGAGCAT	5579
D	6795	GAGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGAGTCCAGAAATTCCTCGAGCAT	6854
Q	5580	GCCCATATGGGCAAGCCCGGATTTCAACCTCCACATGTTAGATCTCTGSAAGAGACCGGA	5639
D	6855	GCCCATATGGGCGCCCGGATTTCAACCTCCACATGTTAGATCTCTGSAAGAGACCGGA	6914
Q	5640	CTACGTCCCTCAGTGTGTACACGGGTGTTCATTTGCCGCTGACCAAGGCCCTCCGATACC	5699
D	6915	CTACGTCCCTCAGTGTGTGTACACGGGTGTTCATTTGCCGCTGACCAAGGCCCTCCGATACC	6974
Q	5700	ACCTCCAGAGAGAGAGAGAGGTGTTCCTGTACAGATCTACCGTGTCTTTCGCTTGGC	5759
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QY	5760	GGACCTGGCCACAAGACCTTGGCAGCTCCGAATGTGTGGCCCTCCAGACACGGCCACAGGC	5813
Db	7035	GGAGCTTGCTACTAAGACCTTGGCAGCTCCGAATGTGTGGCCCTCCAGACACGGCCACAGGC	7094
QY	5820	AAGGCCTCTCTCAGCAGCCCTCCACAGCAGCGCAGCGGGGATCCGAGCTTGAAGTCGA	5879
Db	7095	GAGCGCCCTTCTGTGACCAAGCCCTCCAGCAGCGGTGACAAAGGATCCGAGCTTGAAGTCGA	7154
QY	5880	CTCTCCATGCCCCCTTGAAGGGGAGCCGGGGGATCCCGATCTCCACGACGGGTCTGTG	5939
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QY	5940	GCTTACCGTAAGCAGCAGAGCTAGTAGAGCAGTCGTCTGTCTCTGATGTCTTACACATG	5999
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QY	6060	GAGCAACCTTGTGCTCGCTCAGCACAACCTTGTATGTGTACACATCTCGCAGCGCAAG	6119
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QY	6240	GGAACCCGTAGCTGAGCGCCCCCACATTTGGCGAGTGTCAATTTGGCTATGGGCGAAA	6299
Db	7515	GGAACCCGTAGAGCTGAGCGCCCCCACATTTGGCGAATTCAMATTTGGCTATGGGCGAAA	7574
QY	6300	GGACGTCCGGAACCTATTCAGCAGAGCGCGTTAACACATCCGCTCCGTGTGAGAGACTT	6358
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QY	6360	GCTGGAACACACTGAGACCAATTAAGACACACATCATAGGCAAAAATGAGCTTTCTG	6419
Db	7635	GCTGGAACACACTGAGACCAATTAAGACACACATCATAGGCAAAAATGAGCTTTCTG	7694
QY	6420	CCCTCCACAGAGAAAGGGGGCCGCAAGCCAGCTCGCTTATGTATTTCCAGATTTGGG	6479
Db	7695	TCCTCCACAGAGAAAGGGGGCCGTAAGCCAGCCGCTTATGTATTTCCAGATTTGGG	7754
QY	6480	GGTTGCTGTGTGCGAGAAATAGGCGCTTACAGATGTGTGTCCACCTCCCTCAGACGCT	6538
Db	7755	AGTCGGTGTGTGCGAGAAATAGGCGCTTATGATGTGTGTCCACCTCCCTCAGAGTGT	7814
QY	6540	GATGGGCTTTCATACGAGATTCATCTCTCTGACAGCGGGTGAATCTCTGCTGTGA	6599
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QY	6660	AACGGTCACTGAGATGACATCCGTGTGAGAGTCAATCTACCAATGTTGTGACTTGGC	6713
Db	7935	AACGGTCACTGAGAGACATCCGTGTGAGAGTCAATTTACCAATGTGTGACTTGGC	7994
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QY	6780	GACTAATCTTAAGGGCAAAACTGGGCTATCGCGGTGCCGCGGAGGGGTGTACTGAC	6833
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Mon Jun 2 08:44:25 2003

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Db	8115	GACTAGCTGGGTAACACACCTCACATGTACTTGAAGGCTCTCGAGCTGTGAGCTGC	8174
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OY	7080	CTCTCTCAATGTGTCAAGTGGCGAGCATGTGATCTGGCAAAAAGGGTATCTATCCACCG	7139
Db	8355	TTCTCCCAATGTGTCTGGTGGCCACGATCATCAGCAAAAGGGTATCTATCCACCG	8414
OY	7140	TGACCCACCAACCCCTCTTGCGGGGCTCGTGGGAGACAGCTAGACACTCCAGTCAA	7199
Db	8415	TGATCCACCAACCCCTTACACAGGGCTCGTGGGAGACAGTATACACTCCAGTTAA	8474
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OY	7260	GACTCATTTCTTCCATCTCTTACTAGGAGACACTTGAAGAGCCCTAGATTGTCA	7319
Db	8535	GACTCATTTCTTCCATCTCTTACTAGGAGACACTTGAAGAGCCCTGGACTGTCA	8594
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OY	7380	CCATGGGCTTAGGCCATTTCACCCATAGTACTCTCCAGGTGAGATCAATAGGGTGGC	7439
Db	8655	CCATGGGCTTAGGCCATTTCACCTCACTAGTACTCTCCAGGTGAGATCAATAGGGTGGC	8714
OY	7440	TTTCATGCTCTAGGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAAGCATCGGCCAAG	7499
Db	8715	TTTCATGCTCTAGGAAACTTGGGGTACCACTTGAGCACTTACCTCGATCATTTGAACGACT	8774
OY	7500	TGTCCGGCTAGGGTACTGTGCCAGGGGGGAGGGGTGCGACTTGGGCAATGACTCTT	7559
Db	8775	CGTCCGGCTAGGGTACTGTGCCAGGGAGGAGGAGGGCGCCACTTGTGGCAATGACTCTT	8834
OY	7560	CAACTGGGAGTAAAGCAAGCTCAACACTACTCCATCCCGGCTGGCTCCCACTTGA	7619
Db	8835	CAACTGGGAGTAAAGCAAGCTCAACACTACTCCAAATCCCGGCTGGCTCCCACTTGA	8894
OY	7620	TTTATTCACAGCGTGTGTTGTTGTTGTTACAGCGGGGGAGACATATATCAAGGCTCTCG	7699
Db	8895	CTTGTTCGAGTGTGTTGTTGTTGTTGTTACAGCGGGGGAGACATATATCAAGGCTCTCG	8954
OY	7680	TGCCCCAGCCCGCTGGTTCATGTGTGCTACTCTACTTCTGTGTAGGGGTAGGCATCTA	7739
Db	8955	TGCCCCAGCCCGCTGGTTCATGTGTGCTACTCTACTTCTGTGTAGGGGTAGGCATCTA	9014
OY	7740	TCTACTCCCAACCGA 7755	
Db	9015	CTGCTCTCCCAACCGA 9030	

Search completed: May 31, 2003, 16:43:22
Job time : 372 secs